

Db 61 QIRVDFRKRDKGIPGRVATIEIDPNRNSANIALINYADGERR-YIIAAKGLBEVGQIYs 118
 QY 121 GAAADTKVGNALPQNTIPIVGTVVHNIEULKPGKGEGQTLARSAGASAQVIGKEGRVYLRLRS 180
 Db 119 GAAADTKVGNALPQNTIPIVGTVVHNIEULKPGKGEGQTLARSAGASAQVIGKEGRVYLRLNS 178
 QY 181 GEYRMILSTCRATIGOVGNLQHELVNVKAGRSRWKGIRTPYRGSVNPNNDPHGGCGR 240
 Db 179 GEYRMILATCRATIGOVGNENQHELINCKAGRSRWMGKRPYTRGSVNPNDPHGGCGRK 238
 QY 241 APIGRPSMSPMGKPTLGSKTRGKSSDKLIVGRCK 279
 Db 239 APIGRKSPSMSPMGKPTLGKYKTRKNNNSDKFIVRRCKK 277

RESULT 15
 ID ADS44623 standard; protein; 277 AA.
 XX AC ADS44623;
 DT 02-DEC-2004 (first entry)
 XX DE Bacterial polypeptide #23053.
 XX Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW Pathogen tolerance; pest tolerance; Plant disease resistance;
 KW cell cycle pathway modification; Plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX Bacteria.
 OS XX US2003233675-A1.
 PN XX US2003233675-A1.
 PD 18-DEC-2003.
 XX 20-FEB-2003; 2003US-00369493.
 PR 21-FEB-2002; 2002US-0360039P.
 XX 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 PI Cao Y., Hinkle GJ, Slater SC, Chen X., Goldman BS;
 XX DR; 2004-061375/06.
 XX
 PT New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 PS Claim 1; SEQ ID NO 23053; 122pp; English.
 XX
 CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a plant with the
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,

PI	Buchrieser C, Frangeul L, Couve E, Rusniok C, Fehl H, Dehoux P;	KW	Antisense; prokaryotic essential gene; cell proliferation; drug design.
PI	Chebutani F, Nedjazi H, Glaser P, Cossart P;	XX	
PI	Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;	OS	Listeria monocytogenes.
PI	Dominguez-Bernal G, Garrido-Garcia P, Tellez-Martinez A, Amend A;	XX	
PI	Chakraborty T, Donnan E, Bain T, Berche P, Charbit A, Durant L;	XX	WO200277183-A2.
PI	Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;	XX	
PI	Madienio E, De Pablo B, Weiland J, Entian K, Hauf J;	PD	03-OCT-2002.
PI	Rose M, Voss H;	XX	
XX	DR 2002-010914/01.	PR 21-MAR-2002; 2002NO-US009107.	
XX	PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides.	PR 21-MAR-2001; 2001US-00815242.	
PT	PT	PR 06-SEP-2001; 2001US-00948993.	
PT	PT	PR 25-OCT-2001; 2001US-0342923P.	
XX	PS 6-MAR-2002; 2002US-00072851.	PR 08-FEB-2002; 2002US-00072851.	
XX	PS 21-MAR-2002; 2002NO-US009107.	PR 06-MAR-2002; 2002US-032699P.	
XX	DR 2003-022926/02.	XX	
PA	(ELITTA PHARM INC.	PA	
XX	PA	XX	
CC	The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitam B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences	PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Yamamoto R, Forsyth RA, Xu HH;	Zyskind JW;
CC	XX	PI Wall D, Trawick JD, Carr GU;	
CC	XX	DR ACA36412.	
PS	PS Claim 25; SEQ ID NO 60466; 1766pp. English.	PS Claim 25; SEQ ID NO 60466; 1766pp. English.	
XX	XX	XX	
CC	The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:	CC PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation programs to isolate candidate molecules for rational drug discovery programs.	
CC	CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or its gene product lies in a pathway in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences		
XX	XX	XX	
SQ	Sequence 277 AA;	SQ Sequence 277 AA;	
Qy	Query Match 82.6%; Score 1203; DB 5; Length 277;	Qy Query Match 82.6%; Score 1203; DB 6; Length 277;	
Qy	Best Local Similarity 82.4%; Pred. No. 6.5e-112;	Best Local Similarity 82.4%; Pred. No. 6.5e-112;	
Matches 230;	Matches 230;	Matches 230;	
Conservative 20;	Conservative 20;	Conservative 20;	
Indels 27;	Indels 27;	Indels 27;	
Gaps 1;	Gaps 1;	Gaps 1;	
Db	1 MAIKKYKPTINGRNMNTSLDPAEITKTPBKSLIKPLPKAGRNNOGLTVRHGGGKIKR 60	Db 1 MAIKKYKPTINGRNMNTSLDPAEITKTPBKSLIKPLPKAGRNNOGLTVRHGGGKIKR 60	
Qy	1 MAIKKYKPTINGRNMNTSLDPAEITKTPBKSLIKPLPKAGRNNOGLTVRHGGGKIKR 60	Qy 1 MAIKKYKPTINGRNMNTSLDPAEITKTPBKSLIKPLPKAGRNNOGLTVRHGGGKIKR 60	
Db	1 QYRVIDFERNKDGINAKVDIQTDPNSANIALVYADGBKRIVHCKLAPRKLGLEVGQIVES 120	Db 1 QYRVIDFERNKDGINAKVDIQTDPNSANIALVYADGBKRIVHCKLAPRKLGLEVGQIVES 120	
Qy	61 QYRVIDFERNKDGINAKVDIQTDPNSANIALVYADGBKRIVHCKLAPRKLGLEVGQIVES 120	Qy 61 QYRVIDFERNKDGINAKVDIQTDPNSANIALVYADGBKRIVHCKLAPRKLGLEVGQIVES 120	
Db	61 QYRVIDFERNKDGINAKVDIQTDPNSANIALVYADGBKRIVHCKLAPRKLGLEVGQIVES 118	Db 61 QYRVIDFERNKDGINAKVDIQTDPNSANIALVYADGBKRIVHCKLAPRKLGLEVGQIVES 118	
Qy	121 GAEADTKVGNALPLONIPTVGYTIVVHNIELKPKGKGQQIATSGASAOVGLKGKYLIRLS 180	Qy 121 GAEADTKVGNALPLONIPTVGYTIVVHNIELKPKGKGQQIATSGASAOVGLKGKYLIRLS 180	
Db	119 GAEADIKVNALEILKDIPVGTNRIEMPKGKGQLVRSAGTSQVLGKEKGKVLIRUNS 178	Db 119 GAEADIKVNALEILKDIPVGTNRIEMPKGKGQLVRSAGTSQVLGKEKGKVLIRUNS 178	
Qy	181 GEVRMILSTORATIGQVNQIQLHELYNVNGKAGRSEWKGIRTPRTVRSVWNPNHDPHGGGGGR 240	Qy 181 GEVRMILSTORATIGQVNQIQLHELYNVNGKAGRSEWKGIRTPRTVRSVWNPNHDPHGGGGGR 240	
Db	179 GEVRMILATCRATIGQVNQIQLHELYNVNGKAGRSEWKGIRTPRTVRSVWNPNHDPHGGGGK 238	Db 179 GEVRMILATCRATIGQVNQIQLHELYNVNGKAGRSEWKGIRTPRTVRSVWNPNHDPHGGGGK 238	
Qy	241 APIGRSPSPMSPWGKPTLKGKTRGKSSDKLIVLGRKCK 279	Qy 241 APIGRSPSPMSPWGKPTLKGKTRGKSSDKLIVLGRKCK 279	
Db	239 APIGRKSPMSPWGKPTLGYKTRKNNNSDKFIVRRCK 277	Db 239 APIGRKSPMSPWGKPTLGYKTRKNNNSDKFIVRRCK 277	
XX	XX	XX	
Qy	Sequence 277 AA;	Qy Sequence 277 AA;	
Qy	Result 14	Qy Result 14	
ID	ABU32542	ID ABU32542	
XX	standard; protein: 277 AA.	XX standard; protein: 277 AA.	
AC	ABU32542;	AC ABU32542;	
XX	19-JUN-2003 (first entry)	XX 19-JUN-2003 (first entry)	
DE	Protein encoded by Prokaryotic essential gene #18069.	DE Protein encoded by Prokaryotic essential gene #18069.	
XX	61 QYRVIDFERNKDGINAKVDIQTDPNSANIALVYADGBKRIVHCKLAPKGLEYGVIVES 120	XX 61 QYRVIDFERNKDGINAKVDIQTDPNSANIALVYADGBKRIVHCKLAPKGLEYGVIVES 120	

RESULT 12
ABU42626
 ID ABU42626 standard; protein; 277 AA.
 XX
 AC ABU42626;
 XX 19-JUN-2003 (first entry)
 DT
 DE Protein encoded by Prokaryotic essential gene #28153.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS *Staphylococcus epidermidis*.
 XX WO20071183-A2.
 PN
 XX PD 03-OCT-2002.
 XX
 XX 21-MAR-2002; 2002WO-US009107.
 PP
 XX 21-MAR-2001; 2001US-00815242.
 PR
 PR 06-SEP-2001; 2001US-00948933.
 PR
 PR 25-OCT-2001; 2001US-0342923P.
 PR
 PR 08-FEB-2002; 2002US-00072851.
 PR
 PR 06-MAR-2002; 2002US-03162699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX DR; 2003-059926/02.
 DR N-PSDB; AC46496.
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 Claim 25; SEQ ID NO 70550; 1766pp; English.
 XX
 PA The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of

CC the gene product or that has an activity against a biological pathway;
 CC required for proliferation, or that inhibits cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC on a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the Gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences

XX SQ Sequence 277 AA:
 Query Match 94.3%; Score 1373; DB 6;
 Best Local Similarity 93.9%; Pred. No. 5; e-129;
 Matches 262; Conservative 11; Mismatches 4; Indels 2; Gaps 1;

QY	1 MAIKKYPITNGRNMNTSLDPAEITKTPEKSILKPLPKAGRNNQKLTRHHGGHKR	60
Db	1 MAIKKYPITNGRNMNTSLDPAEITKTPEKSILKPLPKAGRNNQKLTRHHGGHKR	60
QY	61 QYRVIDFGRNKDGIAKVDSIODYDPNSANTIALVUVYADGEKRYHCTAPKGLEVGIVES	120
Db	61 QYRVIDFGRNKDGIAKVDSIODYDPNSANTIALVUVYADGEKRYHCTAPKGLEVGIVES	118
QY	121 GARADTKVGNALPLQNTPVGTVHNLKPGKGQIARSAGASAQVIGKEGVYKLRLRS	180
Db	119 GARADTKVGNALPLQNTPVGTVHNLKPGKGQIARSAGASAQVIGKEGVYKLRLRS	178
QY	181 GEVRMILSTCRATIGQVNGLQHELNVNGKAQRGRMKGTRPTGSMVNPNDIPHGGSEGR	240
Db	179 GEVRMILSTCRATIGQVNGLQHELNVNGKAQRGRMKGTRPTGSMVNPNDIPHGGSEGR	238
QY	241 APIGRSPSPMSPWGKPTLGKTRGKSSDKLIVGRKKK 279	
Db	239 APIGRSPSPMSPWGKPTLGKTRGKSSDKLIVGRKKK 277	

XX

Query Match 94.3%; Score 1373; DB 6;
 Best Local Similarity 93.9%; Pred. No. 5; e-129;
 Matches 262; Conservative 11; Mismatches 4; Indels 2; Gaps 1;

QY	1 MAIKKYPITNGRNMNTSLDPAEITKTPEKSILKPLPKAGRNNQKLTRHHGGHKR	60
Db	1 MAIKKYPITNGRNMNTSLDPAEITKTPEKSILKPLPKAGRNNQKLTRHHGGHKR	60
QY	61 QYRVIDFGRNKDGIAKVDSIODYDPNSANTIALVUVYADGEKRYHCTAPKGLEVGIVES	120
Db	61 QYRVIDFGRNKDGIAKVDSIODYDPNSANTIALVUVYADGEKRYHCTAPKGLEVGIVES	118
QY	121 GEAADTKVGNALPLQNTPVGTVHNLKPGKGQIARSAGASAQVIGKEGVYKLRLRS	180
Db	119 GEAADTKVGNALPLQNTPVGTVHNLKPGKGQIARSAGASAQVIGKEGVYKLRLRS	178
QY	181 GEVRMILSTCRATIGQVNGLQHELNVNGKAQRGRMKGTRPTGSMVNPNDIPHGGSEGR	240
Db	179 GEVRMILSTCRATIGQVNGLQHELNVNGKAQRGRMKGTRPTGSMVNPNDIPHGGSEGR	238
QY	241 APIGRSPSPMSPWGKPTLGKTRGKSSDKLIVGRKKK 279	
Db	239 APIGRSPSPMSPWGKPTLGKTRGKSSDKLIVGRKKK 277	

XX

RESULT 13
 ABB49366
 ID ABB49366 standard; protein; 277 AA.
 XX
 AC ABB49366;
 XX DT 05-FEB-2002 (first entry)
 XX
 DB Listeria monocytogenes protein #2070.
 XX
 KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
 KW vitamin B12; bacterial infection; disease.
 XX
 OS Listeria monocytogenes.
 XX
 XX WO200177335-A2.
 XX
 XX 18-OCT-2001.
 XX
 XX 11-APR-2001; 2001WO-FR001118.
 XX
 XX 11-APR-2000; 2000FR-00004629.
 XX
 PA (INSP) INST PASTEUR.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a gene in an operon required for proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

Sequence 277 AA:

Query Match 94.8%; Score 1380; DB 6; Length 277;
Best Local Similarity 94.3%; Pred. No. 1.1e-129; Mismatches 11; Matches 263; Conservative 3; Indels 2; Gaps 1;

Qy	1 MAIKKYKPTINGRNNMTSLDPAKITKTPEKSILKPKAGRNNOCKLITVHHGSGHKR	60
Db	1 MALKKYKPTINGRNNMTSLDPAEIKTKSTPEKSILQPLPKAGRNNOCKLITVHHGSGHKR	60
Qy	61 QTRVIDFKNRDGIDNAKVDISQDPNSANIAUYYADGERIYHICAPKGLBVQIVTES	120
Db	61 QTRVIDFKNRDGIDTAKDISQDPNSANIAUYYADGERR-YTAPKGLOVQIVTES	118
Qy	121 GAEADTIVGNALPLQNTPVGTVYHNTIELPKGKGQIATRSAGASAQVIGKEGVYLIRLS	180
Db	119 GADADIVGNALPLQNTPVGTVYHNTIELPKGKGQIATRSAGASAQVIGKEGVYLIRLS	178
Qy	181 GEVRMILSTCRATIGQVNLNQHELVNYKGAKSRMKGKTRPTGSMVNPNDPHGGSGCR	240
Db	179 GEVRMILSTCRATIGQVNLNQHELVNYKGAKSRMKGKTRPTGSMVNPNDPHGGSGCR	238
Qy	241 APIGRPSPMSPWKGKPTLGKTRGKSSDKLIVRGRKK	279
Db	239 APIGRPSPMSPWKGKPTLGKTRGKSSDKLIVRGRKK	277

Sequence 279 AA:

Query Match 94.4%; Score 1375; DB 5; Length 279;
Best Local Similarity 93.5%; Pred. No. 3.6e-129; Mismatches 12; Conservative 4; Indels 8 2; Gaps 1;

Qy	1 MAIKKYKPTINGRNNMTSLDPAEIKTKTPERSILQPLPKAGRNNOCKLITVHHGSGHKR	60
Db	3 MALKKYKPTINGRNNMTSLDPAEIKTKTPERSILQPLPKAGRNNOCKLITVHHGSGHKR	62
Qy	61 QTRVIDFKNRDGIDNAKVDISQDPNSANIAUYYADGERIYHICAPKGLBVQIVTES	120
Db	63 QTRVIDFKNRDGIDTAKDISQDPNSANIAUYYADGERR-YTAPKGLOVQIVTES	120
Qy	121 GAEADTIVGNALPLQNTPVGTVYHNTIELPKGKGQIATRSAGASAQVIGKEGVYLIRLS	180
Db	121 GAEADTIVGNALPLQNTPVGTVYHNTIELPKGKGQIATRSAGASAQVIGKEGVYLIRLS	180
Qy	181 GEVRMILSTCRATIGQVNLNQHELVNYKGAKSRMKGKTRPTGSMVNPNDPHGGSGCR	240
Db	181 GEVRMILSTCRATIGQVNLNQHELVNYKGAKSRMKGKTRPTGSMVNPNDPHGGSGCR	240
Qy	241 APIGRPSPMSPWKGKPTLGKTRGKSSDKLIVRGRKK	279
Db	241 APIGRPSPMSPWKGKPTLGKTRGKSSDKLIVRGRKK	279

RESULT 9
ID ABP38415 standard; protein: 279 AA.
XX AC ABP38415;
XX DT 24-JUL-2002 (first entry)
XX DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3260.
XX KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.
XX OS Staphylococcus epidermidis.

RESULT 10
ID ADS07076 standard; protein: 279 AA.
XX AC ADS07076;
XX DT 04-NOV-2004 (first entry)
XX DE Staphylococcus epidermidis polypeptide seqid 6371.
XX KW recombinant expression vector; infection; computer readable medium; computer based system.

the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 277 AA;

Query Match	Score 1412;	DB 6;	Length 277;	
Best Local Similarity	97.0%;	Pred. No.	6.9e-133;	
Matches	274;	Conservative	1;	Mismatches 2;
Indels	2;	Gaps	1;	
SQ	Sequence 277 AA;			
Qy	1 MAIKKYKPTINGRNMNTSLDAEITKTTPPEKSLLKPLPKAGRNNOGLTLVREHGGHKR	60		
Db	1 MAIKKYKPTINGRNMNTSLDAEITKTTPPEKSLLKPLPKAGRNNOGLTLVREHGGHKR	60		
Qy	61 QYRVIDFKRNDGGINAKYDSIQDPNSANIALVYADGEKRYHCIAPKGLEVQIVES	120		
Db	61 QYRVIDFKRNDGGINAKYDSIQDPNSANIALVYADGEKRY-HIAPKGLEVQIVES	118		
Qy	121 GAEADTKVGNALPLQNIPIGTVHNIELKPGKQQIARSAGASAQVLGKEGVTLIRLS	180		
Db	119 GAEADTKVGNALPLQNIPIGTVHNIELKPGKQQIARSAGASAQVLGKEGVTLIRLS	178		
Qy	181 GEVRMILSTCRATIGQVNLIQHELNVNGKAQRSRWKIGRPTVRSVNPNDHPHGGEGR	240		
Db	179 GEVRMILSTCRATIGQVNLIQHELNVNGKAQRSRWKIGRPTVRSVNPNDHPHGGEGR	238		
Qy	241 APIGRPSPMSPWKGKPTLGSKTRGKSSDKLIVGRKCK	279		
Db	239 APIGRPSPMSPWKGKPTLGSKTRGKSSDKLIVGRKCK	277		

RESULT 7

ABM72939 ABM72939 standard; protein; 277 AA.

XX ABM72939;

XX DT 20-NOV-2003 (first entry)

XX Staphylococcus aureus protein #2179.

XX Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;

XX enzymatic assay; antibiotic target.

OS Staphylococcus aureus.

XX PN WO200294868-A2.

XX PD 28-NOV-2002.

XX PF 27-MAR-2002; 2002WO-IB002637.

XX PR 27-MAR-2001; 2001GB-00007661.

XX PA (CHIR-) CHIRON SPA.

XX PI Masiignani V, Mora M, Scarselli M;

XX DR 2003-120786/11.

XX DR N-PSDB; ACPF4499.

XX WPI; SEQ ID NO 4358; 49pp; English.

XX The invention relates to novel genes and encoded proteins from

CC Staphylococcus aureus. A composition comprising the S. aureus protein,

PT nucleic acid encoding the protein, or an antibody to the protein, is

PT useful as a pharmaceutical, particularly as a vaccine for treating or

PT preventing infection due to Staphylococcus bacteria, specifically an

CC infection caused by S. aureus. The composition is particularly useful for

CC treating or preventing sepsis in a patient. The composition can also be

CC used for diagnostics. The protein is also used in an assay for enzymatic

CC studies and as a target for antibiotics. This sequence represents one of

CC the novel S. aureus proteins of the invention

XX SQ Sequence 277 AA;

CC	infection or preventing sepsis in a patient. The composition can also be
CC	used for diagnostics. The protein is also used in an assay for enzymatic
CC	studies and as a target for antibiotics. This sequence represents one of
CC	the novel S. aureus proteins of the invention
XX	SQ Sequence 277 AA;

Query Match	97.0%;	Score 1412;	DB 6;	Length 277;
Best Local Similarity	98.2%;	Pred. No.	6.9e-133;	
Matches	274;	Mismatches	1;	
Indels	2;	Gaps	1;	
SQ	Sequence 277 AA;			

Query Match	97.0%;	Score 1412;	DB 6;	Length 277;
Best Local Similarity	98.2%;	Pred. No.	6.9e-133;	
Matches	274;	Mismatches	1;	
Indels	2;	Gaps	1;	
SQ	Sequence 277 AA;			

Query Match	97.0%;	Score 1412;	DB 6;	Length 277;
Best Local Similarity	98.2%;	Pred. No.	6.9e-133;	
Matches	274;	Mismatches	1;	
Indels	2;	Gaps	1;	
SQ	Sequence 277 AA;			

Query Match	97.0%;	Score 1412;	DB 6;	Length 277;
Best Local Similarity	98.2%;	Pred. No.	6.9e-133;	
Matches	274;	Mismatches	1;	
Indels	2;	Gaps	1;	
SQ	Sequence 277 AA;			

Query Match	97.0%;	Score 1412;	DB 6;	Length 277;
Best Local Similarity	98.2%;	Pred. No.	6.9e-133;	
Matches	274;	Mismatches	1;	
Indels	2;	Gaps	1;	
SQ	Sequence 277 AA;			

Query Match	97.0%;	Score 1412;	DB 6;	Length 277;
Best Local Similarity	98.2%;	Pred. No.	6.9e-133;	
Matches	274;	Mismatches	1;	
Indels	2;	Gaps	1;	
SQ	Sequence 277 AA;			

Query Match	97.0%;	Score 1412;	DB 6;	Length 277;
Best Local Similarity	98.2%;	Pred. No.	6.9e-133;	
Matches	274;	Mismatches	1;	
Indels	2;	Gaps	1;	
SQ	Sequence 277 AA;			

Query Match	97.0%;	Score 1412;	DB 6;	Length 277;
Best Local Similarity	98.2%;	Pred. No.	6.9e-133;	
Matches	274;	Mismatches	1;	
Indels	2;	Gaps	1;	
SQ	Sequence 277 AA;			

Query Match	97.0%;	Score 1412;	DB 6;	Length 277;
Best Local Similarity	98.2%;	Pred. No.	6.9e-133;	
Matches	274;	Mismatches	1;	
Indels	2;	Gaps	1;	
SQ	Sequence 277 AA;			

Query Match	97.0%;	Score 1412;	DB 6;	Length 277;
Best Local Similarity	98.2%;	Pred. No.	6.9e-133;	
Matches	274;	Mismatches	1;	
Indels	2;	Gaps	1;	
SQ	Sequence 277 AA;			

Query Match	97.0%;	Score 1412;	DB 6;	Length 277;
Best Local Similarity	98.2%;	Pred. No.	6.9e-133;	
Matches	274;	Mismatches	1;	
Indels	2;	Gaps	1;	
SQ	Sequence 277 AA;			

Query Match	97.0%;	Score 1412;	DB 6;	Length 277;
Best Local Similarity	98.2%;	Pred. No.	6.9e-133;	
Matches	274;	Mismatches	1;	
Indels	2;	Gaps	1;	
SQ	Sequence 277 AA;			

Query Match	97.0%;	Score 1412;	DB 6;	Length 277;
Best Local Similarity	98.2%;	Pred. No.	6.9e-133;	
Matches	274;	Mismatches	1;	
Indels	2;	Gaps	1;	
SQ	Sequence 277 AA;			

Query Match	97.0%;	Score 1412;	DB 6;	Length 277;
Best Local Similarity	98.2%;	Pred. No.	6.9e-133;	
Matches	274;	Mismatches	1;	
Indels	2;	Gaps	1;	
SQ	Sequence 277 AA;			

Query Match	97.0%;	Score 1412;	DB 6;	Length 277;
Best Local Similarity	98.2%;	Pred. No.	6.9e-133;	
Matches	274;	Mismatches	1;	
Indels	2;	Gaps	1;	
SQ	Sequence 277 AA;			

Query Match	97.0%;	Score 1412;	DB 6;	Length 277;
Best Local Similarity	98.2%;	Pred. No.	6.9e-133;	
Matches	274;	Mismatches	1;	
Indels	2;	Gaps	1;	
SQ	Sequence 277 AA;			

Query Match	97.0%;	Score 1412;	DB 6;	Length 277;
Best Local Similarity	98.2%;	Pred. No.	6.9e-133;	
Matches	274;	Mismatches	1;	
Indels	2;	Gaps	1;	
SQ	Sequence 277 AA;			

Query Match	97.0%;	Score 1412;	DB 6;	Length 277;

<tbl_r cells="5" ix="2" maxcspan="1" maxrspan="1

DE Pathogen specific antigen related staphylococcal protein SEQ ID No 222.
 XX Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV;
 KW hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen;
 KW auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
 KW autoimmune disease; HIV; hepatitis.
 XX Staphylococcus sp.
 OS WO200259148-A2.
 XX PI Meinke A, Nagy B, Von Ahsen U, Klade C, Henics T, Zauner W,
 PI Minh DB, Vytvyska O, Btz H, Dryla A, Weichhart T, Haffner M;
 PI Tempelmaier B;
 DR WPI: 2003-075410/07.
 XX PT Identifying, isolating and producing hyperimmune serum-reactive antigens
 PT from a pathogen, for preparing vaccine or medicament for treating or
 preventing e.g. staphylococcal infections, comprises providing antibody
 preparation.
 XX PS Example 7; Page 186; 252pp; English.
 XX The invention relates to a novel method for identifying, isolating and
 CC producing hyperimmune serum-reactive antigens from a pathogen, tumour,
 CC allergen, a tissue or host prone to auto-immunity, where the antigens are
 CC used in a vaccine, comprises providing antibody preparation from a plasma
 CC pool of a type of animal, or individual sera with antibodies against the
 CC specific pathogen, tumour, allergen, tissue or host prone to auto-
 CC immunity. The hyperimmune serum-reactive antigens comprising any of the
 CC 62 sequences of 53-2261 amino acids fully defined in the specification,
 CC or their hyperimmune fragments are useful for the manufacture of a
 CC pharmaceutical preparation, particularly a vaccine against staphylococcal
 CC infections or colonization against S. aureus or S. epidermidis. The
 CC preparation of antibodies is useful for the manufacture of a medicament
 CC for treating or preventing staphylococcal infections or colonisation
 CC against S. aureus or S. epidermidis. The antibody preparations may also
 CC be used for diagnostic and imaging purposes. Other conditions that can be
 CC treated include cancer, autoimmune diseases or infections caused by viral
 CC (e.g. HIV, hepatitis A, B or C), fungal or protozoan pathogens. This
 CC sequence represents a staphylococcal protein relating to the method for
 CC identifying and producing pathogen specific antigens of the invention
 XX Sequence 277 AA;

Qy 97.0%; Score 1412; DB 6; Length 277;
 Best Local Similarity 98.2%; Pred. No. 6.9e-13; Mismatches 1; Indels 2; Gaps 1;
 Matches 274; Conservative 1;

Db 1 MAIKKYKPTINGRNNTSLDFAIBTKTPEKSILKPLPKAGRNNOQKLTVRHGGHKR 60
 1 MAIKKYKPTINGRNNTSLDFAIBTKTPEKSILKPLPKAGRNNOQKLTVRHGGHKR 60
 Qy 61 QRVIDFKRNRGINKARYSDIQYDPNTSANTIALVYADGERIYHCAPKGLEVQIVTES 120
 61 QRVIDFKRNRGINKARYSDIQYDPNTSANTALVYADGERIYHCAPKGLEVQIVTES 120
 Db 61 QRVIDFKRNRGINKARYSDIQYDPNTSANTALVYADGERIYHCAPKGLEVQIVTES 118
 121 GAEADTKVGNALPQLNPVGTVHNIELKPGIGGQIARSAGASAQVLGKEGVYLRLRS 180
 119 GAEADTKVGNALPQLNPVGTVHNIELKPGIGGQIARSAGASAQVLGKEGVYLRLRS 178
 Qy 181 GEVRMLSTCRATIGQVNGLQHLVNYGKAQRGRSRWKGTRPVTYRGSMVNPHGGGBGR 240
 Db 179 GEVRMLSTCRATIGQVNGLQHLVNYGKAQRGRSRWKGTRPVTYRGSMVNPHGGGBGR 238

Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6									
OM protein - protein search, using SW model										
Run on: June 9, 2005, 15:48:59 ; Search time 161 Seconds (without alignments) 670.225 Million cell updates/sec										
Title: US-09-839-695B-13										
Perfect score: 1456										
Sequence: 1 MATKVKPITNGRNNMTSLD.....KTRRGKSSDKLIVRGRKKK 279										
Scoring table: BLOSUM62										
Gapext: 0.5										
Searched: 2105692 seqs, 386760381 residues										
Total number of hits satisfying chosen parameters:	2105692									
Minimum DB seq length: 0										
Maximum DB seq length: 2000000000										
Post-processing: Minimum Match 0%										
Maximum Match 100%										
Listing first 45 summaries										
Database : A_Geneseq_16Dec04:*										
1: GeneseqP1990s:*										
2: GeneseqP1990s:*										
3: GeneseqP2000s:*										
4: GeneseqP2001s:*										
5: GeneseqP2002s:*										
6: GeneseqP2003as:*										
7: GeneseqP2003bs:*										
8: GeneseqP2004s:*										
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.										
SUMMARIES										
Result No.	Score	Query Match	Length	DB ID	Description					
1	1412	97.0	277	3 AAY70416	Aay70416	Staphylococcus aureus ribosomal protein RPL2 from S10-spC operon of	XX	PR	25-AUG-1998;	99WO-US019298.
2	1412	97.0	277	4 AUJ6656	AuJ6656	Staphylococcus aureus ribosomal protein RPL2 from S10-spC operon of	XX	PA	25-AUG-1998;	99US-00139234.
3	1412	97.0	277	4 AUJ7174	AuJ7174	Staphylococcus aureus ribosomal protein RPL2 from S10-spC operon of	XX	PA	25-AUG-1998;	99US-00139234.
4	1412	97.0	277	4 AUJ34212	AuJ34212	Staphylococcus aureus ribosomal protein RPL2 from S10-spC operon of	XX	PA	25-AUG-1998;	99US-00139234.
5	1412	97.0	277	6 ABJ19004	ABJ19004	Pathogen	XX	PA	25-AUG-1998;	99US-00139234.
6	1412	97.0	277	6 ABU15836	ABU15836	Protein e	XX	PA	25-AUG-1998;	99US-00139234.
7	1412	97.0	277	6 ABM72939	ABM72939	Staphylococcus aureus ribosomal protein RPL2 from S10-spC operon of	XX	PA	25-AUG-1998;	99US-00139234.
8	1380	94.8	277	6 ABU33554	ABU33554	Protein e	XX	PA	25-AUG-1998;	99US-00139234.
9	1375	94.4	279	5 ABP38415	ABP38415	Staphylococcus aureus ribosomal protein RPL2 from S10-spC operon of	XX	PA	25-AUG-1998;	99US-00139234.
10	1375	94.4	279	8 ADS07076	ADS07076	Staphylococcus aureus ribosomal protein RPL2 from S10-spC operon of	XX	PA	25-AUG-1998;	99US-00139234.
11	94.3	277	6 ABJ19022	ABJ19022	Pathogen	XX	PA	25-AUG-1998;	99US-00139234.	
12	1373	94.3	277	6 ABU2626	ABU2626	Protein e	XX	PA	25-AUG-1998;	99US-00139234.
13	1203	82.6	277	5 ABBA9366	ABBA9366	Listeria	XX	PA	25-AUG-1998;	99US-00139234.
14	1203	82.6	277	6 ABU32542	ABU32542	Protein e	XX	PA	25-AUG-1998;	99US-00139234.
15	1163	79.9	277	8 ADS44623	ADS44623	Bacterial	XX	PA	25-AUG-1998;	99US-00139234.
16	1154	79.3	276	8 ADS28071	ADS28071	Bacterial	XX	PA	25-AUG-1998;	99US-00139234.
17	1121	77.0	276	4 AUJ6394	AUJ6394	Protein e	XX	PA	25-AUG-1998;	99US-00139234.
18	1120	76.9	276	4 AUJ4962	AUJ4962	Protein e	XX	PA	25-AUG-1998;	99US-00139234.
19	1120	76.9	276	6 ABU14500	ABU14500	Protein e	XX	PA	25-AUG-1998;	99US-00139234.
20	1117	76.7	276	5 ABP28608	ABP28608	Streptococcus	XX	PA	25-AUG-1998;	99US-00139234.
21	1112	76.4	274	4 AUJ33423	AUJ33423	Enterococcus	XX	PA	25-AUG-1998;	99US-00139234.
22	1108	76.1	277	4 AUJ7607	AUJ7607	Streptococcus	XX	PA	25-AUG-1998;	99US-00139234.
23	1108	76.1	277	4 AUJ37946	AUJ37946	Streptococcus	XX	PA	25-AUG-1998;	99US-00139234.
24	1108	76.1	277	6 ABU00552	ABU00552	S. pneumoniae	XX	PA	25-AUG-1998;	99US-00139234.
25	1108	76.1	277	6 ABP81521	ABP81521	Streptococcus	XX	PA	25-AUG-1998;	99US-00139234.
ALIGNMENTS										
RESULT 1										
ID AAY70416	standard; protein; 277 AA.									
AC AAY70416;										
XX DT 21-JUN-2000	(first entry)									
XX DE Staphylococcus aureus ribosomal protein RPL2.										
XX AX AAY70416										
XX DT 21-JUN-2000	(first entry)									
XX DE Staphylococcus aureus ribosomal protein RPL2.										
XX AX AAY70416;										
XX DT 21-JUN-2000	(first entry)									
XX DE Staphylococcus aureus ribosomal protein RPL2.										
XX AX AAY70416;										
XX DT 21-JUN-2000	(first entry)									
XX DE Staphylococcus aureus ribosomal protein RPL2.										
XX AX AAY70416;										
XX DT 21-JUN-2000	(first entry)									
XX DE Staphylococcus aureus ribosomal protein RPL2.										
XX AX AAY70416;										
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XX DE Staphylococcus aureus ribosomal protein RPL2.										
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XX DE Staphylococcus aureus ribosomal protein RPL2.										
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XX DE Staphylococcus aureus ribosomal protein RPL2.										
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XX DE Staphylococcus aureus ribosomal protein RPL2.										
XX AX AAY70416;										
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XX DE Staphylococcus aureus ribosomal protein RPL2.										
XX AX AAY70416;										
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XX DE Staphylococcus aureus ribosomal protein RPL2.										
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XX DE Staphylococcus aureus ribosomal protein RPL2.										
XX AX AAY70416;										
XX DT 21-JUN-2000	(first entry)									
XX DE Staphylococcus aureus ribosomal protein RPL2.										
XX AX AAY70416;										
XX DT 21-JUN-2000	(first entry)									
XX DE Staphylococcus aureus ribosomal protein RPL2.										

Qy 238 EGRAPIGRSPSPWGPKEPTLAKKTRGCKSPLDKLIVGRK 278
 Db 239 EGQPIGPKAALPWPCKALGYTRDNCKSSTKLIVRRK 279

RESULT 14
AE2332 50S ribosomal protein L2 [Imported] - *Nostoc* sp. (strain PCC 7120)
C; Species: *Nostoc* sp. PC 7120
A; Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C; Accession: AB2332
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi, N.; Nakazaki, N.; Shimpoo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. strain PCC 7120
A; Reference number: AB1807; MUID:2155285; PMID:11759840
A; Accession: AB2332
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-287 <KOB>
A; Cross-references: UNIPROT:Q8YI2; GB:BA000019; PIDN:BAE75911.1; PID:91713347; GSPDB:Q

C; Experimental source: strain PCC 7120
C; Genetics:
A; Gene: rpl2
C; Superfamily: ribosomal protein L2/L8

Query Match 61.6%; Score 897; DB 2; Length 287;
 Best Local Similarity 62.6%; Pred. No. 1.5e-63;
 Matches 174; Conservative 35; Mismatches 67; Indels 2; Gaps 1;

Qy 1 MAIKKYKPTINGRRNMTSLDAPIATKCTPEKSLLKPLPKKAAGRNNQGKLTYRHGGGHKR 60
 Db 1 MGTSRSYBTPSTQRQVTSDFAIIKTEPEKSLLTYYGRAGSRNNQCRITSSRGCCGHKR 60

Qy 61 QIRVIFKRNDKGINAKVDISIQDNPNSANIALUVVADGERKTYHCTAPKGLEVGIVES 120
 Db 61 LYRIIDFGRDRSIPATVIAEYDPNMRNARIALVSYEDGER-YILHPNNLKVGTVIA 118

Qy 121 GAAADTKVGNALPLQNIQVGTQVHNNEIKPGRGQIARSAGASAQVIGKEGRXVLRSL 180
 Db 119 GPFSPIEDGNALPLGLTSVHNELKAGRGQIYRSGATAQVVAKEGVYVTLKPS 178

Qy 181 GEFVRMLSTCRAFTIGQVGNLQHFLVNYKGAGRGSRKGTRPTVGRGSVMNPNDPHGGGAEGR 240
 Db 179 GEYVLIRECYATTIGQVNTDAMNLNSACKAGRNRWKGRPKYRGSMVNPNVDPHGGGEGR 238

Qy 241 APIGRPSMSPKCKPTLCKKTRGKSSDKLIVGRKK 278
 Db 239 APIGRSGEVTPNCKPTLGAKTRPKKASSKLIRRKK 276

RESULT 15
C82915 ribosomal protein L2 UU34 [Imported] - *Ureaplasma urealyticum*
C; Species: *Ureaplasma urealyticum*
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 07-Jul-2003
R; Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
Submitted to GenBank, February 2000
A; Description: The complete sequence of *Ureaplasma urealyticum*: Alternate views of a minor reference sequence.
A; Reference number: A82870
A; Accession: C82915
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-279 <GLA>
A; Cross-references: GB:AE002123; GB:AF22894; NID:96899229; PIDN:AAF30643.1; GSPDB:GN001
A; Experimental source: serovar 3; biovar 1
C; Genetics:
A; Gene: rpl2; UU34
A; Generic code: SGC3
C; Superfamily: ribosomal protein L2/L8

Qy	181	GEVRMILSTCRATIGQVNGLQHELVNVGKAGRGSRWKGTRPTVRSVMMNPNDIPHGGGEGR	240	A; Molecule type: DNA A; Residues: 1-6, N'; 8-18, 'TBCSSLFPNNQKIA', 31-35, 'GG', 38-41, 'TA', 44-46, 'KS', 49-51, 'SS', 54-25
Db	179	GEVKVLNCRATIGEENSYKLINYGRAGKGRFLGTRPTVRSVMMNPNDIPHGGGEGR	238	C; Genetics: C; Superfamily: ribosomal protein L2/L8 C; Keywords: protein biosynthesis; ribosome
Qy	241	APIGRPSPMSPMGKPTLGKTRACKSSDKLIVYRGKK	278	
Db	239	APIGRKSPTMPWCGKARGYKTRDKKASVNLIRRRTK	276	
RESULT 11				
B97285		ribosomal protein L2 [Imported] - Clostridium acetobutylicum		
C; Species: Clostridium acetobutylicum				
C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004				
C; Accession: B97285				
R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.				
J; Bacteriol. 183, 4823-4832, 2001				
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1c				
A; Reference number: A96900; MUID:21359325; PMID:21359325;				
A; Accession: B97285				
A; Status: preliminary				
A; Molecule type: DNA				
A; Residues: 1-277 <KUR>				
A; Cross-references: UNIPROT:Q97E11; GB:AE001437; PIDN:AAK81069..1; PID:915026196; GSPPDB:Q				
A; Experimental source: Clostridium acetobutylicum ATCC824				
C; Genetics:				
A; Gene: CAC13130				
C; Superfamily: ribosomal protein L2/L8				
Query Match	66.6%	Score 969; DB 2;	Length 277;	
Best Local Similarity	65.2%	Pred. No. 2, 9e-69;		
Matches	182;	Conservative	37; Mismatches	58; Indels 2; Gaps 1;
RESULT 13				
A99585				
50S ribosomal protein L2 [Imported] - Mycoplasma pulmonis (strain UAB CTIP)				
C; Species: Mycoplasma pulmonis				
C; Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004				
C; Accession: A99585				
R; Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.				
Nucleic Acids Res. 29, 2145-2153, 2001				
A; Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmo				
A; Reference number: A99512; PMID:11353084				
A; Accession: A99585				
A; Status: preliminary				
A; Molecule type: DNA				
A; Residues: 1-281 <KUR>				
A; Cross-references: UNIPROT:Q98PY4; GB:AL445566; PID:914090000; PIDN:CAC13758..1; GSPPDB:Q				
A; Experimental source: strain UAB CTIP				
C; Genetics:				
A; Gene: MYPU_5850				
C; Superfamily: ribosomal protein L2/L8				
Query Match	63.2%	Score 920.5; DB 2;	Length 281;	
Best Local Similarity	64.4%	Pred. No. 2e-65;		
Matches	181;	Conservative	37; Mismatches	58; Indels 5; Gaps 3;
RESULT 12				
R5YM2C				
ribosomal protein L2 - Mycoplasma capricolum				
C; Species: Mycoplasma capricolum				
C; Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004				
C; Accession: S02834; S05072				
R; Ohkubo, S.; Muro, A.; Kawauchi, Y.; Yamao, F.; Obama, S.				
Mol. Genet. 210, 314-322, 1987				
A; Title: The ribosomal protein gene cluster of Mycoplasma capricolum.				
A; Accession: S02834				
A; Molecule type: DNA				
A; Residues: 1-281 <OKH>				
A; Cross-references: UNIPROT:P10133; EMBL:X06414				
R; Muto, A.				
Submitted to the EMBL Data Library, January 1989				
A; Reference number: S05072				
A; Accession: S05072				

Db	1 MGIRVYKPTTNGRNMTSLDFAITTSPEKSLVALSKAAGRNNNGRITVHQGGSHKR	60	R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic Genome Res. 11, 731-753, 2001 A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp
Qy	61 QYRVIDPFRNKDGINAKVDSIQDPNSANTIALVYVADGERKRYHCTAPKGLEVGIVES	120	A;Reference number: A86625 ; MUID: 21235186 ; PMID: 11337471
Db	61 FYRLDIFCRNKDNVEAVVKTIEDPNSANTIALVHTDGVKA-YTAPKGLEVGIVRS	118	A;Accession: H86886 A;Status: Preliminary
Qy	121 GAAATDKVGNALPLQNIPVGTVVHNIELKPGRGQIARSAGASAQVLGKEGVYLRLRS	180	A;Molecule type: DNA A;Cross-references: UNIPROT:Q96176 ; PIDN:AAK06194.1 ; GSPDB:GT
Db	119 GPEADIKVGNALPLQNIPVGTLTHNIELKPGRGELTRAGASAQVLGSEGK 240	1	A;Experimental source: strain IL1403 C;Genetics:
Qy	181 GEVRMLSTCRATTGQVNLYLQHLLVNGKAGSRWKIGIRPTYGSVNPNDPHGGEGR	279	A;Gene: rp1B
Db	179 GEVRMLGTCRATVGVVNEQHGLVNLKGAGSRWKIGIRPTYGSVNPNDPHGGEGK	238	C;Superfamily: ribosomal protein L2/L8
RESULT 8			
Qy	241 APIGRPSMSPKPTGKCKTRGKSSDKLIVTRGRKK	279	Query Match Score 73.6%; DB 2; Length 276;
Db	239 APIVGRKAPSTPMSKPKALGKTRNKKAKSDKLIVRRNEK	277	Best Local Similarity 74.8%; Pred. No. 2-1e-20; Mismatches 24; Indels 2; Gaps 1;
RESULT 9			
Qy	505 ribosomal protein L2 - Streptococcus pneumoniae (strain R6)	1	Query Match Score 1072; DB 2; Length 276;
C;Species: Streptococcus pneumoniae			C;Species: mycoplasma-like organism, MLG8
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004			C;Date: 06-Oct-1994 #sequence_revision 25-Apr-1997 #text_change 07-Jul-2003
C;Accession: G-97895			C;Accession: B5-547
R;Hoskins, J.A.; Alborn, Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; Dehoff, B.S.; E			R;Lim, P.O.; Sears, B.B.
Y, P.; Sun, P.M.; Winkler, M.E.			FEMS Microbiol. Lett. 68, 71-73, 1991
J. Bacteriol. 183, 5709-5717, 2001			A;Title: Sequence of the ribosomal protein genes rps12 and rps19 from a plant-pathogen
J;Authors: Yang, Y.; Young, Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;			A;Reference number: A54547 ; MUID: 9212050 ; PMID: 11544234
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.			A;Accession: B5-547
A;Cross-references: UNIPROT:Q97SV2 ; PIDN:AAK98995.1 ; PIDN:91			A;Status: Preliminary
A;Accession: G97895			A;Molecule type: DNA
A;Status: Preliminary			A;Note: sequence inconsistent with nucleotide translation
A;Molecule type: DNA			A;Title: DNA sequence of the ribosomal protein genes rps12 and rps19 from a plant-pathogen
A;Residues: 1-277 <KOR>			C;Superfamily: ribosomal protein L2/L8
A;Cross-references: UNIPROT:Q97SV2 ; PIDN:AAK98995.1 ; PIDN:91			A;Gene: rp1B
C;Genetics:			Query Match Score 971; DB 2; Length 276;
Db	1 MGIRVYKPTTNGRNMDSLDFAITTKTPEKSLKPLPKAGRNNOQLTVRHGGHHKR	60	Best Local Similarity 68.0%; Pred. No. 2e-69; Mismatches 57; Indels 2; Gaps 1;
Qy	1 MAIKKYKPTTNGRNMDSLDFAITTKTPEKSLKPLPKAGRNNOQLTVRHGGHHKR	60	Query Match Score 971; DB 2; Length 276;
Db	1 MGIRVYKPTTNGRNMDSLDFAITTSPEKSLVALSKAAGRNNNRITVHQGGHKR	60	Best Local Similarity 68.0%; Pred. No. 2e-69; Mismatches 57; Indels 2; Gaps 1;
Qy	61 QYRVIDPFRNKDGINAKVDSIQDPNSANTIALVYVADGERKRYHCTAPKGLEVGIVES	120	Query Match Score 971; DB 2; Length 276;
Db	61 FYRLDIFCRNKDNVEAVVKTIEDPNSANTIALVHTDGVKA-YTAPKGLEVGIVRS	118	Best Local Similarity 68.0%; Pred. No. 2e-69; Mismatches 57; Indels 2; Gaps 1;
Qy	121 GAAATDKVGNALPLQNIPVGTVVHNIELKPGRGQIARSAGASAQVLGKEGVYLRLRS	180	Query Match Score 971; DB 2; Length 276;
Db	119 GPEADIKVGNALPLQNIPVGTLTHNIELKPGRGELTRAGASAQVLGSEGK 240	1	Best Local Similarity 68.0%; Pred. No. 2e-69; Mismatches 57; Indels 2; Gaps 1;
Qy	179 GEVRMLGTCRATVGVVNEQHGLVNLKGAGSRWKIGIRPTYGSVNPNDPHGGEGK	238	Query Match Score 971; DB 2; Length 276;
Db	241 APIGRPSMSPKPTGKCKTRGKSSDKLIVTRGRKK	279	Best Local Similarity 68.0%; Pred. No. 2e-69; Mismatches 57; Indels 2; Gaps 1;
Db	239 APIVGRKAPSTPMSKPKALGKTRNKKAKSDKLIVRRNEK	277	Query Match Score 971; DB 2; Length 276;
RESULT 9			
H86886	505 ribosomal protein L2 [Imported] - Lactococcus lactis subsp. lactis	1	Query Match Score 1072; DB 2; Length 276;
C;Species: Lactococcus lactis subsp. lactis			C;Species: mycoplasma-like organism, MLG8
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004			C;Date: 06-Oct-1994 #sequence_revision 25-Apr-1997 #text_change 07-Jul-2003
C;Accession: H86886			C;Accession: B5-547

C;Accession: AE1403	R;Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Bagnero, F.; Berche, P.; Bloecker, R.; Dominguez-Bernal, G.; Duchaude, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihi, H.D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001	ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of <i>Listeria</i> species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669	A;Accession: AE1403
C;Superfamily: ribosomal protein L2/L8	A;Status: preliminary
A;Molecule type: DNA	A;Residues: 1-277 <GLA>
A;Cross-references: UNIPROT:P60426; GB:NC_003210; PIDN:CADD00707.1; PID:g16412117; GSPDB:1	A;Experimental source: strain EGD-e
C;Genetics:	A;Gene: rp1B
Query Match Score 82 %; Length 277;	Best Local Similarity 82 %; Pred. No. 9.1e-88;
Matches 230; Conservative 20; Mismatches 27; Indels 2; Gaps 1;	Matches 230; Conservative 20; Mismatches 27; Indels 2; Gaps 1;
Qy 1 MAIKYKPTINGRMRNTSDFAEITKTTPERKSLLKPLKKAGRNNNGQKLTVRHGGGGHKR 60	Db 1 MAIKYKPTINGRMRNTSDFAEITKTTPERKSLLKPLKKAGRNNNGQKLTVRHGGGGHKR 60
Qy 61 QYRVIDFKEKNDGIMAKUDS1QYDPRNSANTALVYADGEKRYCHIAPKCLEVGIVES 120	Db 61 QYRVIDFKEKNDGIVGRVATEYDPMRSANTALVYADGEKRYCHIAPKCLEVGIVES 120
Qy 121 GAAEADTKVGNALPLONTIPGVTVHANIBLKPKGGQTARSAGASAVQLGKESKVKYLRLRS 180	Db 119 GAAEADTKVGNALPLONTIPGVTVHANIBLKPKGGQTARSAGASAVQLGKESKVKYLRLRS 178
Qy 181 GEYRMILSTCRATIGSGVNLQHELYNVKGAGRGSRNLKIRPTVGSYMNPNDPHGGGGEGR 240	Db 179 GEVRMLATRATICGQVNBSFHNLINKGAGRGSRNLKIRPTVGSYMNPNDPHGGGGEGK 238
Qy 241 APIGRKSPMSPWGKPTLGIKTRRGKSSDKLIVRKCK 279	Db 239 APIGRKSPMSPWGKPTLGIKTRRGKSSDKLIVRKCK 277
RESULT 3	AD1779
ribosomal protein L2 [imported] - <i>Listeria innocua</i> (strain Clip11262)	C;Species: <i>Listeria innocua</i>
C;Dre: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004	C;Accession: AD1779
R;Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Bagnero, F.; Berche, P.; Bloecker, R.; Dominguez-Bernal, G.; Duchaude, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihi, H.D.; Jones, L.M.; Karst, U.	A;Authors: Kreft, J.; Kuhn, M.; Kunst, P.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of <i>Listeria</i> species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669	A;Accession: AD1779
C;Status: preliminary	A;Molecule type: DNA
A;Residues: 1-277 <GLA>	A;Cross-references: UNIPROT:P60425; GB:AL592022; PIDN:GAC98004.1; PID:g16415314; GSPDB:1
A;Experimental source: strain Clip11262	A;Experimental source: strain Clip11262
C;Genetics:	C;Genetics:
Query Match Score 82 %; Length 277;	Best Local Similarity 82 %; Pred. No. 9.1e-88;
Matches 230; Conservative 20; Mismatches 27; Indels 2; Gaps 1;	Matches 230; Conservative 20; Mismatches 27; Indels 2; Gaps 1;
Qy 1 MAIKYKPTINGRMRNTSDFAEITKTTPERKSLLKPLKKAGRNNNGQKLTVRHGGGGHKR 60	Qy 1 MAIKYKPTINGRMRNTSDFAEITKTTPERKSLLKPLKKAGRNNNGQKLTVRHGGGGHKR 60

Db	1	MAIKCKYKPTINGRRNMTSSLDAEITTPPEKSLLPKKGQIARSGASQVLGEGKTYVLRNLS	60
Qy	61	QYRVIDFKRDGGINAKVDSIQYDPNRSANIALVVADGEKRYHCAPKGLGEVQIVIES	120
Db	61	QYRVIDFKRDGGINAKVDSIQYDPNRSANIALVVADGEKRYHCAPKGLGEVQIVIES	118
Db	121	GAEADTKVGNALPQNIPVGTVVHNELKPKGKGGQIARSGASQVLGEGKTYVLRNLS	180
Db	119	GAEADTKVGNALPQNIPVGTVVHNELKPKGKGGQIARSGASQVLGEGKTYVLRNLS	178
Qy	181	GEVRMLISTRATIGOVGNLQHELVNGKAGRSRWKGIRPTYRGSVVNPNNDPHGGGEGGR	240
Db	179	GEVRMLISTRATIGOVGNLQHELVNGKAGRSRWKGIRPTYRGSVVNPNNDPHGGGEGGR	238
Qy	241	APIGRGSPMSWPWKGKPTLGKTRRGKSSDKL1YVRREKK	279
Qy	241	APIGRGSPMSWPWKGKPTLGKTRRKONNSDKF1YVRREKK	277
Db	239	APIGRGSPMSWPWKGKPTLGKTRRKONNSDKF1YVRREKK	277
RESULT 4			
	F69694	ribosomal protein L2 (BL2) _rp1B - Bacillus subtilis	
C:	Species: Bacillus subtilis		
C:	Date: 05-Dec-1997 # sequence_revision 05-Dec-1997 #text_change 09-Jul-2004		
C:	Accession: F69694		
R:	Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.C.; Ehrlicher, S.D.; Emmerling, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrer, A.; Hilpert, H.; Holsappel, S.; Horono, S.; Hull, M.; Kurita, K.; Lapidus, A.; Laub, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Ogawa, K.; Ogiwara, C.; Oudega, B.; Parro, V.; Pohl, T.M.; Po, Y.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Schleicher, S.; Schroeter, R.; Scoffone, F.; Seiguchi, J.; Sekowska, A.; Akeuchi, M.; Tamakoshi, A.; Yamane, K.; Yamamoto, H.; Yipat, A.; Yitbarek, P.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yipat, A.; Yoshikawa, H.R.; Zumstein, B.; Danchin, A.		
A:	Article: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. Reference number: A69580; PMID: 98044033; PMID: 9334377		
A:	Accession: F69694		
A:	Status: Preliminary; nucleic acid sequence not shown; translation not shown		
A:	Molecule type: DNA		
A:	Residues: 1-277 <KUN>		
A:	Cross-references: UNIPROT:P42919; GB:Z99104; PID:NID:009126; PID:NID:009126		
A:	Experimental source: strain 168		
C:	Genetics:		
A:	Gene: rp1B		
C:	Superfamily: ribosomal protein L2/L8		
Query Match	79.9%	Score 1163; DB 2; Length 277;	
Best Local Similarity	79.9%	Pred. No. 1..3e-84; Indels 2; Gaps 1;	
Matches	223;	Conservative 19; Mismatches 35;	
Db	1	MAIKCKYKPTINGRRNMTSSLDAEITTPPEKSLLPKKGQIARSGASQVLGEGKTYVLRNLS	60
Qy	61	QYRVIDFKRDGGINAKVDSIQYDPNRSANIALVVADGEKRYHCAPKGLGEVQIVIES	120
Db	61	QYRVIDFKRDGGINAKVDSIQYDPNRSANIALVVADGEKRYHCAPKGLGEVQIVIES	118
Qy	121	GAEADTKVGNALPQNIPVGTVVHNELKPKGKGGQIARSGASQVLGEGKTYVLRNLS	180
Db	119	GAEADTKVGNALPQNIPVGTVVHNELKPKGKGGQIARSGASQVLGEGKTYVLRNLS	178
Qy	181	GEVRMLISTRATIGOVGNLQHELVNGKAGRSRWKGIRPTYRGSVVNPNNDPHGGGEGGR	240
Db	179	GEVRMLISTRATIGOVGNLQHELVNGKAGRSRWKGIRPTYRGSVVNPNNDPHGGGEGGR	238
Qy	241	APIGRGSPMSWPWKGKPTLGKTRRGKSSDKL1YVRREKK	279

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 9, 2005, 15:57:59 ; Search time 40 Seconds
Perfect score: 1456 (without alignments)
Sequence: 1 MAIKKPKITNGRNMNTSLD.....KTRRGKKSDDKLIVRGKKK 279

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : PIR_79;*

1: pir1;*

2: pir2;*

3: pir3;*

4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1412	97.0	277	2 B90022	50S ribosomal prot
2	1203	82.6	277	2 AE1403	ribosomal protein
3	1163	82.6	277	2 AD1719	ribosomal protein
4	1154	79.9	277	2 F69694	ribosomal protein
5	1154	79.3	276	2 T44386	ribosomal protein
6	1125	77.3	275	1 R5BS2F	ribosomal protein
7	1108	76.1	277	2 G95024	ribosomal protein
8	1108	76.1	277	2 G97895	50S ribosomal prot
9	1072	73.6	276	2 H6886	50S ribosomal prot
10	971	66.7	276	2 B54547	ribosomal protein
11	969	66.6	277	2 B97285	ribosomal protein
12	958	65.8	281	1 R5YMC	ribosomal protein
13	920.5	63.2	281	2 A99585	50S ribosomal prot
14	897	61.6	287	2 AE2332	50S ribosomal prot
15	885	61.5	279	2 B82915	ribosomal protein
16	885	60.8	275	2 B75534	ribosomal protein
17	880	60.4	280	2 C70642	probable ribosomal protein
18	876	60.2	274	2 CB2059	ribosomal protein
19	871.5	59.9	276	2 A72250	ribosomal protein
20	862.5	59.2	274	1 R5EB2Y	50S ribosomal prot
21	862.5	59.2	274	2 AB0026	ribosomal protein
22	855	58.7	275	1 R5KT2	ribosomal protein
23	855	58.7	280	2 T45367	ribosomal protein
24	846	58.1	275	2 S78273	ribosomal protein
25	843	57.9	277	2 D82005	50S ribosomal prot
26	842	57.8	276	2 S77449	ribosomal protein
27	842	57.8	277	2 C81231	50S ribosomal prot
28	838	57.6	273	2 B83116	50S ribosomal prot
29	837.5	57.5	273	1 R5EC2	50S ribosomal prot

ALIGNMENTS

RESULT 1

B90022

50S ribosomal protein L2 [Imported] - *Staphylococcus aureus* (strain N315)

C:Species: *Staphylococcus aureus*

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: B90022

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Inoue, R.; Kaijo, C.; Sekimizu, K.; iC; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.

A;Reference number: A99758; PMID:21311952; PMID:1418146

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-277 <KRB>

A;Cross-references: UNIPROT:P60432; GB:BA000018; PID:g13702047; PID:BA433339.1; GSPDB:GN

A;Experimental source: strain N315

C;Genetics:

A;Accession: B90022

A;Status: preliminary

A;Superfamily: ribosomal protein L2/L8

Query Match

97.0%

Score 1412;

DB 24;

Length 277;

Best Local Similarity

98.2%;

Prod. No. 2.7e-104;

Mismatches 2;

Indels 8;

Gaps 1;

Matches 274;

Conservative

1

MAIKKYKPTINGRNMNTSLDFABITKTTPPEKSUJKPLPKAGENNOQGLTVRHGGHKR

60

1 MAIKKYKPTINGRNMNTSLDAEITKTTPPEKSUJKPLPKAGENNOQGLTVRHGGHKR

60

1 MAIKKYKPTINGRNMNTSLDFABITKTTPPEKSUJKPLPKAGENNOQGLTVRHGGHKR

60

61 QYRVIDFCKRKDGIAKVDIYQDPNRSDANIALVYVADGEKRTYHCAPKGLEVGQLYVES

120

61 QYRVIDFCKRKDGIAKVDIYQDPNRSDANIALVYVADGEKRTY-HTAPKGLEVGQIVES

118

121 GAEADTKVGNALPQNIPVGTVHNIEELKPKGKGQIARSAGASAQVLKEGKVYLIRLRS

180

119 GAEADTKVGNALPQNIPVGTVHNIEELKPKGKGQIARSAGASAQVLKEGKVYLIRLRS

178

181 GEVRMILSTCRATIGQVGRNLQHELVNKGAGRGSRWKGIRPTVGRGSVNPNNDPHGGGBR

240

179 GEVRMILSTCRATIGQVGNLQHELVNKGAGRGSRWKGIRPTVGRGSVNPNNDPHGGGBR

238

241 APIGRPSPMSPWPKTLQKTRIGKSSDKLIVGRICK

279

239 APIGRPSPMSPWPKTLQKTRIGKSSDKLIVGRICK

277

ribosomal protein L2 [Imported] - *Listeria monocytogenes* (strain EGD-e)

C:Species: *Listeria monocytogenes*

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

Best Local Similarity 78.8%, Pred. No. 2e-82; Matches 219; Conservative 26; Mismatches 31; Indels 2; Gaps 1									
Db 1 AIKKYKPSNSGRRGMGTTSDPAEITTDKEKSLLAPLHKGGRNNQKLTVRGGGHHRQ	60	Qy 62 YRVIDFKRNDGINAKVDSIQDPNRSANTALVVYADGERKRYHCIAPKGLLEYQOIVESG	121	Qy 1 MAIKKYKPTINGRRNMNTSLDFAEITTKTPBEKSLLKPLPKAGRNQGKLTVRHGGHHR	60	Db 61 YRVIDFKRDKDGPGRVATEVDPNRSANTALINADGER--YILAPKQIQVTEIMSG	118	Db 1 MAIKKFKPNSGRNMNTSDFAEITTDPEKSLLSPRERGRGNQGKLTVRHGGHHR	60
Qy 62 AEDTIVKGNPLPQNIPVGTVVNLBKEKGQQTARSAGASAOYLGREGKXVLIRLSG	181	Qy 61 QYRVIDFKRNDGINAKVDSIQDPNRSANTALVVYADGERKRYHCIAPKGLLEYQIVES	120	Db 119 PEADIKVGNPLPQNIPVGTVVNLBKEKGQQTARSAGASAOYLGREGKXVLIRLSG	178	Db 61 QYRVIDFKRDKDGPGRVATEVDPNRSANTALVVYADGERK--YIAPKQIKYQEIES	118	Db 120 GAEADTKYGNALPLQNPVGTWVHNIELPKPGKGQLARSAGASAOVLGKEKGKVYLRLRS	180
Qy 182 EVMILSTCATATIGVGNLRELNVKGARSRNKGIRPTVRGSVMNPNDHPGGGEGRA	241	Qy 121 GAEADTKYGNALPLQNPVGTWVHNIELPKPGKGQLARSAGASAOVLGKEKGKVYLRLRS	180	Db 179 EVMILSACASISGQVNGNECHELINIGKGRSRNKGIRPTVRGSVMNPNDHPGGGEGRA	238	Db 119 GENADICLGNALPLQNPVGTWVHNIELPKPGQQLASAGAEOQILGRBEKTLVRLSS	178	Db 120 GEVRMILSTCRATIGVGNLQHELVNGKAGRSPWKGRPTVRGSVMNPNDHPGGGEGRA	240
Qy 242 PIGRSPMSPWGKPTLGIKTRGKCKSSDKLIVGRKKKK	279	Qy 121 GEVRMILSTCRATIGVGNLQHELVNGKAGRSPWKGRPTVRGSVMNPNDHPGGGEGRA	240	Db 239 PIGRSPMSPWGKPTLGIKTRGKCKSSDKLIVGRKKKK	276	Db 179 GEVRMILSTCRATIGVGNLQHELVNGKAGRSPWKGRPTVRGSVMNPNDHPGGGEGRA	238	Db 241 APTGRSPMSPWGKPTLGIKTRGKCKSSDKLIVGRKK	278
AC QBETX9; ID _RL2_OCEIH; STANDARD; PRT; 276 AA.		AC QBETX9; ID _RL2_BACHD; STANDARD; PRT; 276 AA.		AC QBETX9; ID _RL2_BACHD; STANDARD; PRT; 276 AA.		AC QBETX9; ID _RL2_BACHD; STANDARD; PRT; 276 AA.		AC QBETX9; ID _RL2_BACHD; STANDARD; PRT; 276 AA.	
DT 29-MAR-2004 (Rel. 43, Created)		DT 29-MAR-2004 (Rel. 43, Last sequence update)		DT 30-MAY-2000 (Rel. 39, Created)		DT 30-MAY-2000 (Rel. 39, Last sequence update)		DT 30-MAY-2004 (Rel. 45, Last annotation update)	
DT 29-OCT-2004 (Rel. 45, Last annotation update)		DT 50S ribosomal protein L2.		DE 50S ribosomal Protein L2.		DE 50S ribosomal Protein L2.		DE 50S ribosomal Protein L2.	
DB GN		Name=rpLB; Order=locusName=BH0137;		GN Name=rpLB; Order=locusName=BH0137;		GN Name=rpLB; Order=locusName=BH0137;		GN Name=rpLB; Order=locusName=BH0137;	
OC OS		Bacteria: Firmicutes; Bactillales; Bacillaceae; Bacteria; Bacillus.		OS Bacteria: Firmicutes; Bactillales; Bacillaceae; Bacteria; Bacillus.		OS Bacteria: Firmicutes; Bactillales; Bacillaceae; Bacteria; Bacillus.		OS Bacteria: Firmicutes; Bactillales; Bacillaceae; Bacteria; Bacillus.	
NCBI_TaxID=182710;		[1]		NCBI_TaxID=86665;		NCBI_TaxID=86665;		NCBI_TaxID=86665;	
OX RN		SEQUENCE FROM N.A.		OX RN		OX RN		OX RN	
RC STRAIN=HTB831 / DSM 14371 / JCM 11309;		RT SEQUENCE FROM N.A.		RC STRAIN=C-125 / JCM 9153;		RC STRAIN=C-125 / JCM 9153;		RC STRAIN=C-125 / JCM 9153;	
RX MEDLINE=2007-067; PubMed=12353706; DOI=10.1093/nar/gkf526;		RT SEQUENCE FROM N.A.		RX MEDLINE=9205008; PubMed=10192928;		RX MEDLINE=9205008; PubMed=10192928;		RX MEDLINE=9205008; PubMed=10192928;	
RA Takanami H., Takaki Y., Uchiyama I.;		RT SEQUENCE FROM N.A.		RA Takanami H., Nakagawa K., Hirama C., Inoue A., Horikoshi K.;		RA Takanami H., Nakagawa K., Hirama C., Inoue A., Horikoshi K.;		RA Takanami H., Nakagawa K., Hirama C., Inoue A., Horikoshi K.;	
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments".		RT SEQUENCE FROM N.A.		RT "Sequence analysis of a 32-kb region including the major ribosomal RNA genes clusters from alkaliophilic Bacillus sp. strain C-125.";		RT "Sequence analysis of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."		RT "Sequence analysis of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."	
RL CC -1 FUNCTION: One of the primary rRNA binding proteins. Required for association of the 30S and 50S subunits to form the 70S ribosome, for tRNA binding and peptide bond formation. It has been suggested to have peptidyltransferase activity; this is somewhat controversial. Makes several contacts with the 16S rRNA in the 70S ribosome (By similarity). Part of the 50S ribosomal subunit. Forms a bridge to the 30S subunit in the 70S ribosome (By similarity).		CC -1 FUNCTION: One of the primary rRNA binding proteins. Required for association of the 30S and 50S subunits to form the 70S ribosome, for tRNA binding and peptide bond formation. It has been suggested to have peptidyltransferase activity; this is somewhat controversial. Makes several contacts with the 16S rRNA in the 70S ribosome (By similarity).		CC -1 FUNCTION: One of the primary rRNA binding proteins. Required for association of the 30S and 50S subunits to form the 70S ribosome, for tRNA binding and peptide bond formation. It has been suggested to have peptidyltransferase activity; this is somewhat controversial. Makes several contacts with the 16S rRNA in the 70S ribosome (By similarity).		CC -1 FUNCTION: One of the primary rRNA binding proteins. Required for association of the 30S and 50S subunits to form the 70S ribosome, for tRNA binding and peptide bond formation. It has been suggested to have peptidyltransferase activity; this is somewhat controversial. Makes several contacts with the 16S rRNA in the 70S ribosome (By similarity).		CC -1 FUNCTION: One of the primary rRNA binding proteins. Required for association of the 30S and 50S subunits to form the 70S ribosome, for tRNA binding and peptide bond formation. It has been suggested to have peptidyltransferase activity; this is somewhat controversial. Makes several contacts with the 16S rRNA in the 70S ribosome (By similarity).	
RT CC -1 SIMILARITY: Belongs to the ribosomal protein L2P family.		RT CC -1 SIMILARITY: Belongs to the ribosomal protein L2P family.		RT CC -1 SIMILARITY: Belongs to the ribosomal protein L2P family.		RT CC -1 SIMILARITY: Belongs to the ribosomal protein L2P family.		RT CC -1 SIMILARITY: Belongs to the ribosomal protein L2P family.	
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CC DR HSSP; P04257; BAC12078.1; -.		CC DR HSSP; P04257; BAC12078.1; -.		CC DR HSSP; P04257; BAC12078.1; -.		CC DR HSSP; P04257; BAC12078.1; -.		CC DR HSSP; P04257; BAC12078.1; -.	
CC DR HANAP; MF_0120; -; 1.		CC DR HANAP; MF_0120; -; 1.		CC DR HANAP; MF_0120; -; 1.		CC DR HANAP; MF_0120; -; 1.		CC DR HANAP; MF_0120; -; 1.	
CC DR InterPro; IPR00899; Nucleic acid OB.		CC DR InterPro; IPR00899; Nucleic acid OB.		CC DR InterPro; IPR00899; Nucleic acid OB.		CC DR InterPro; IPR00899; Nucleic acid OB.		CC DR InterPro; IPR00899; Nucleic acid OB.	
CC DR InterPro; IPR002121; Ribosomal L2.		CC DR InterPro; IPR002121; Ribosomal L2.		CC DR InterPro; IPR002121; Ribosomal L2.		CC DR InterPro; IPR002121; Ribosomal L2.		CC DR InterPro; IPR002121; Ribosomal L2.	
CC DR InterPro; IPR05880; Ribosomal L2/b/o.		CC DR InterPro; IPR05880; Ribosomal L2/b/o.		CC DR InterPro; IPR05880; Ribosomal L2/b/o.		CC DR InterPro; IPR05880; Ribosomal L2/b/o.		CC DR InterPro; IPR05880; Ribosomal L2/b/o.	
CC DR InterPro; IPR00899; Transl SH3-like.		CC DR InterPro; IPR00899; Transl SH3-like.		CC DR InterPro; IPR00899; Transl SH3-like.		CC DR InterPro; IPR00899; Transl SH3-like.		CC DR InterPro; IPR00899; Transl SH3-like.	
CC DR Pfam; PF00181; Ribosomal L2; 1.		CC DR Pfam; PF00181; Ribosomal L2; 1.		CC DR Pfam; PF00181; Ribosomal L2; 1.		CC DR Pfam; PF00181; Ribosomal L2; 1.		CC DR Pfam; PF00181; Ribosomal L2; 1.	
CC DR TIGRFAMS; TIGR01171; rDNA bact; 1.		CC DR TIGRFAMS; TIGR01171; rDNA bact; 1.		CC DR TIGRFAMS; TIGR01171; rDNA bact; 1.		CC DR TIGRFAMS; TIGR01171; rDNA bact; 1.		CC DR TIGRFAMS; TIGR01171; rDNA bact; 1.	
CC DR PROSITE; PS00467; RIBOSOMAL L2; 1.		CC DR PROSITE; PS00467; RIBOSOMAL L2; 1.		CC DR PROSITE; PS00467; RIBOSOMAL L2; 1.		CC DR PROSITE; PS00467; RIBOSOMAL L2; 1.		CC DR PROSITE; PS00467; RIBOSOMAL L2; 1.	
CC KW Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.		CC KW Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.		CC KW Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.		CC KW Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.		CC KW Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.	
CC SEQUENCE 276 AA;		CC SEQUENCE 276 AA;		CC SEQUENCE 276 AA;		CC SEQUENCE 276 AA;		CC SEQUENCE 276 AA;	
CC DR DR 752/4; 1;		CC DR DR 752/4; 1;		CC DR DR 752/4; 1;		CC DR DR 752/4; 1;		CC DR DR 752/4; 1;	
CC EMBL; AB017508; DR DR 752/4; 1;		CC EMBL; AB017508; DR DR 752/4; 1;		CC EMBL; AB017508; DR DR 752/4; 1;		CC EMBL; AB017508; DR DR 752/4; 1;		CC EMBL; AB017508; DR DR 752/4; 1;	

RA Berka R.M.;
 RT "Complete genome sequence of the industrial bacterium Bacillus licheniformis and comparisons with closely related *Bacillus* species.";
 RT *Genome Biol.* 5:R77-R77 (2004).
 RL AE01733; AAU3910.1.;
 DR EMBL; CP00002; AAU21765.1.;
 KW Ribosomal protein.
 SQ SEQUENCE 277 AA; 30302 MW; A6B7DDE718836870 CRC64;

Query Match Score 1175; DB 2; Length 277;
 Best Local Similarity 80.3%; Pred. No. 6.5e-84;
 Matches 224; Conservative 18; Mismatches 35; Indels 2; Gaps 1;

Qy 1 MAI[KYK]P[ITGGRNMTSIDAETTKTP[EKSLLKPLRKAGENNGKLTIVRHGGH][KR 60
 Db 1 MAI[KYK]P[ITGGRNMTSIDAETTKTP[EKSLLKPLRKAGENNGKLTIVRHGGH][KR 60
 Qy 61 QYRVIDF[KRNKG]INAKYD[SIQDPNRSANIALVYADGEKRYIHCIAPKGL[EVQI[VES 120
 Db 61 QYRIDF[KDQG]PGRVATEYDPNRSANIALINVYDG[EKR--YILPKQI[GVTBIMS 118
 Qy 121 GAA[D]KYGNALPLQ[NPVGTCVHNIELKP[GKQQI[AQSAGASAQVLGKE[GKVL]IPIRS 180
 Db 119 GPEADIKYGNALPLQ[NPVGTCVHNIELKP[GKGSQI[VRSA[GTAQVLGKE[GKVL]IPLNS 178
 Qy 181 GEYRMILSPCRATIGQVNGLQELVNKGAKGRSPWKGIRPTGVS[WNPNDAPHGGEGR 240
 Db 179 GEYRMILSACRATIGQVNGLQELVNKGAKGRSPWKGIRPTGVS[WNPNDAPHGGEGR 238

Qy 241 APIGRPSPMSPW[GKPTLGKCTRKSSKSDKLIVYGRKCK 279
 Db 239 APIGRKSPMSPW[GKPTLGKTRCKNS[KPFIYRRKQK 277

RESULT 12
 RLR2_BACSU STANDARD; PRT; 276 AA.
 AC P42919;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 50S ribosomal protein L2 (BL2).
 GN Name=rpL2; OrderedLocusNames=BSU01190;
 OS Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 NCBI_TaxID=1423;
 OX RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=SGB3;
 RX MEDLINE=98037503; PubMed=9371452;
 RA Li X., Lindahl L., Sha Y., Zengel J.M.;
 RT "Analysis of the *Bacillus* subtilis S10 ribosomal protein gene cluster identifies two promoters that may be responsible for transcription of the entire 15-kilobase S10-spc-alpha cluster.";
 RT *J. Bacteriol.* 179:7046-7054 (1997).
 RN SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=8969501;
 RA Kunst F.; Ogawa N.; Moser I.; Albertini A.M.; Alloni G.;
 RT Bertero M.G.; Bessieres P.; Boilot A.; Borchart S.;
 RA Kawamura P.; Yoshikawa H.; Takahashi H.;
 RT "Sequence analysis of a 50 kb region between *spoOH* and *rrnH* on the *Bacillus subtilis* chromosome.";
 RT *Microbiology* 142:3039-3046 (1996).
 RN SEQUENCE FROM N.A.
 RC MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
 RA Kunst F.; Ogawa N.; Moser I.; Albertini A.M.; Alloni G.;
 RT Bertero M.G.; Bessieres P.; Boilot A.; Borchart S.;
 RA Kawamura P.; Yoshikawa H.; Braun M.; Brignell S.C.; Bron S.;
 RT Brouillet S.; Bruschi C.V.; Caldwell B.; Capuano V.; Carter N.M.;
 RA Choi S.K.; Codani J.J.; Connerton I.F.; Cummings N.J.; Daniel R.A.;

RA Denizot F.; Devine K.M.; Dusterhoff A.; Ehrlich S.D.; Emerson P.T.;
 RA Entian K.-D.; Errington J.; Fabret C.; Ferrari E.; Foulger D.;
 RA Fritz C.; Fujita M.; Fujita Y.; Fuma S.; Galizzi A.; Galleron N.;
 RA Ghim S.Y.; Glaser P.; Goffeau A.; Golightly E.J.; Grandi G.;
 RA Giuseppi G.; Guy B.J.; Haga K.; Haich J.; Harwood C.R.; Henaut A.;
 RA Hilbert H.; Hollappel S.; Hosono S.; Hullu M.F.; Itaya M.;
 RA Jones L.-M.; Joris B.; Karamoto D.; Kasahara Y.; Klaerr-Blanchard M.;
 RA Klein C.; Kobayashi Y.; Koetter P.; Koningsstein G.; Krogh S.;
 RA Kumano M.; Kurita K.; Lapinus A.; Lardinolos S.; Lauber J.;
 RA Lazaravic V.; Lee S.M.; Levine A.; Liu H.; Masuda S.; Mauel C.;
 RA Medina N.; Meliado R.P.; Mizuno M.; Moel D.; Nakai S.;
 RA Noback M.; Noone D.; O'Reilly M.; Osawa A.; Oudega B.;
 RA Park S.H.; Parro V.; Pohl T.M.; Portetelle D.; Porwollik S.;
 RA Prescott A.M.; Presecan E.; Puic P.; Purnell B.; Rapoport G.;
 RA Rey M.; Reynolds S.; Rieger M.; Rivolta C.; Rocha E.; Roche B.;
 RA Rose M.; Sadaie Y.; Sato T.; Scanlan B.; Schleicher S.; Schroeter R.;
 RA Sefcovic F.; Sekiguchi J.; Sekowska A.; Seror S.J.; Servar P.;
 RA Shin B.S.; Soldo B.; Sorokin A.; Tacconi E.; Takagi T.; Takahashi H.;
 RA Takemaru K.; Takeuchi M.; Tamakoshi A.; Tanaka T.; Terpetra P.;
 RA Tognoni A.; Tosato V.; Uchiyama S.; Vandebul M.; Vannier P.;
 RA Vassarotti A.; Viari A.; Wambutt R.; Wedler E.; Wedler H.;
 RA Weitzenecker T.; Winters P.; Wipat A.; Yamamoto H.; Yamane K.;
 RA Yasumoto K.; Yata K.; Yoshida K.; Yoshioka H.P.; Zumstein E.;
 RA Yoshikawa H.; Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus* subtilis.";
 RT *Nature* 390:249-256 (1997).
 CC -|- FUNCTION: One of the primary rRNA binding proteins. Required for association of the 30S and 50S subunits to form the 70S ribosome, for tRNA binding and peptide bond formation. It has been suggested to have peptidyltransferase activity; this is somewhat controversial. Makes several contacts with the 16S rRNA in the 70S ribosome (By similarity).
 CC -|- SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the 30S subunit in the 70S ribosome (By similarity).
 CC -|- SIMILARITY: Belongs to the ribosomal protein L2P family.

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CC DR U43929; AAC45959_1; -;
 DR D50302; BA008834_1; -;
 DR P04257; CAB11895_1; -;
 DR P04257; IRL2.
 DR HSSP; P04257; IRL2.
 DR SubjList; BG1217; rp1B.
 DR HAMAP; MF_01320; -;
 DR InterPro; IPR008994; Nucleic_acid_OB.
 DR InterPro; IPR002171; Ribosomal_L2.
 DR InterPro; IPR005880; Ribosomal_L2_b/o.
 DR InterPro; IPR008991; Transl_SH3_1-like.
 DR Pfam; PF00181; Ribosomal_L2_1.
 DR Pfam; PF03947; Ribosomal_L2_C_1.
 DR TIGRFAMS; TIGR01171; rp1B_bact.
 DR PROSITE; PS00467; RIBOSOMAL_L2_1.
 KW Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.
 FT INIT_MET 0 0
 FT CONFLICT 115 115
 FT CONFLICT 255 255
 FT CONFLICT 261 261
 SQ SEQUENCE 276 AA; 30201 MW; 507BD524B3A29A CRC64;
 Query Match Score 1158; DB 1; Length 276;
 Best Local Similarity 79.5%; Pred. No. 1.e-82;
 Matches 222; Conservative 19; Mismatches 35; Indels 2; Gaps 1;
 QY 2 AIRKKYKPTINGRANMTSLDPABLTKTTPKSLLKPLKKAGRANQGKLTVRHGGHHRQ 61

Page 6

kw	Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.	CC or send an email to license@isb-sib.ch).
sq	SEQUENCE 277 AA; 30213 MW; CB9D5B88492CD84C CRC64;	CC EMBL; AU596173; CAC98004.1; -.
Query Match	94.3%; Score 1373; DB 1; Length 277;	DR PIR; AD1779; AD1779.
Best Local Similarity	93.9%; Pred. No. 2e-99; Matches 262; Conservative 11; Mismatches 4; Indels 2; Gaps 1;	DR List; LIN02278; -.
Qy	1 MAIKKYKPTTNGRNRNMTSLDAETKTTPKESLILKPLPKRAGRNNOQLTRHGGGHR 60	DR HAMAP; MF_01320; -; 1.
Db	1 MALKKYKPTTNGRNRNMTSLDAETKTTPKESLILKPLPKRAGRNNOQLTRHGGGHR 60	DR InterPro; IPR02171; Ribosomal L2.
Qy	61 QYRVIDPFRNKDGIAKYDSIQYDPNRNSANTIALVYVADGEKRYIHCIAPKGLEVGQIVES 120	DR TIGRFAMS; TIGR01171; rplB_bact_1.
Db	61 QYRVIDPFRNKDGIAKYDSIQYDPNRNSANTIALVYVADGEKRYIHCIAPKGLEVGQIVES 118	DR PROSITE; PS00467; RIBOSOMAL L2; 1.
Qy	121 GABADTKVGNALPLQNPVPGTVHNIELKPKGKGQIARSAGASAQVLGKEGVYLRLRS 180	DR complete proteome; Ribosomal L2_b/o.
Db	119 GABADTKVGNALPLQNPVPGTVHNIELKPKGKGQIARSAGASAQVLGKEGVYLRLRS 178	DR SEQUENCE 277 AA; 30505 MW; DD05B8498A5A632 CRC64;
Qy	181 GBYVRMILSTCRATIGQVNGLQHELVAVSKGRSRWKGRPRTGVSVMNPNDPHGGSGGR 240	Query Match 82.6%; Score 1203; DB 1; Length 277;
Db	179 GYRMILSTCRATIGQVNGLQHELVAVSKGRSRWKGRPRTGVSVMNPNDPHGGSGGR 238	Best Local Similarity 82.4%; Pred. No. 4.2e-86; Matches 230; Conservative 20; Mismatches 27; Indels 2; Gaps 1;
Qy	241 APIGRPSPMSPNGKPTLGRKTRGKKSDDKLIVTRGRCK 279	Qy 1 MAIKKYKPTTNGRNRNMTSLDAETKTTPKESLILKPLPKRAGRNNOQLTRHGGGHR 60
Db	239 APIGRPSPMSPNGKPTLGRKTRGKKSDDKLIVTRGRCK 277	Db 1 MAIKKYKPTTNGRNRNMTSLDAETKTTPKESLILKPLPKRAGRNNOQLTRHGGGHR 60
Qy	OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.	Qy 61 QYRVIDPFRNKDGIAKYDSIQYDPNRNSANTIALVYVADGEKRYIHCIAPKGLEVGQIVES 120
OS	Listeria innocua.	Db 61 QYRVIDPFRNKDGIPGKRVATIEDDPNRNSANTIALVYVADGEKRYIHCIAPKGLEVGQIVES 118
OX	Name=plB; OrderedLocusNames=lin2778;	Qy 121 GABADTKVGNALPLQNPVGTVHNIELKPKGKGQIARSAGASAQVLGKEGVYLRLRS 180
RN	NCBI_TaxID=1642;	Db 119 GABADTKVGNALPLQNPVGTVHNIELKPKGKGQIARSAGASAQVLGKEGVYLRLRS 178
RESULT 8	RL2_LISMO	RESULT 9
ID	RL2_LISMO STANDARD; PRT; 277 AA.	RL2_LISMO STANDARD; PRT; 277 AA.
AC	P60425; Q927L0;	AC P60426; Q927L0;
DT	29-MAR-2004 (Rel. 43, Created)	DT 29-MAR-2004 (Rel. 43, Created)
DT	29-MAR-2004 (Rel. 43, Last sequence update)	DT 25-OCT-2004 (Rel. 45, Last annotation update)
DT	29-OCT-2004 (Rel. 45, Last annotation update)	DE 50S ribosomal protein L2.
DE	50S ribosomal protein L2.	DN Name=plB; OrderdLocusNames=lm02629;
GN	Name=plB; OrderedLocusNames=lin2778;	OS Listeria monocytogenes.
OC	Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.	Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX	NCBI_TaxID=1639;	OX NCBI_TaxID=1639;
RN	SEQUENCE FROM N.A.	RN SEQUENCE FROM N.A.
RC	STRAIN=CLIP 11262 / Serovar 6a;	RC STRAIN=BGD-1 / Serovar 1/2a.
RX	MEDLINE=2157279; Published: 1996-06-01; DOI=10.1126/science.1063447;	RX MEDLINE=2157279; PubMed=11679669; DOI=10.1126/science.1063447;
RA	Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,	RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA	Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,	RA Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,
RA	Charbit P., Chetouani F., Couve B., de Darvuar A., Dehoux P.,	RA Charbit P., Chetouani F., Couve B., de Darvuar A., Dehoux P.,
RA	Domanu E., Dominguez-Bernal G., Duchaude E., Durant L., Dussargent O.,	RA Doman E., Dominguez-Bernal G., Duchaude E., Durant L., Dussargent O.,
RA	Entian K.-D., Pahli H., Garcia-del Portillo F., Garrido P.,	RA Entian K.-D., Pahli H., Garcia-del Portillo F., Garrido P.,
RA	Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,	RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA	Jones L.-M., Kaelst U., Kunst F., Kurapkat G.,	RA Jones L.-M., Kaelst U., Kunst F., Kurapkat G.,
RA	Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,	RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA	Remmeli B., Rose M., Perez-Diaz J.-C., Purcell R.,	RA Remmeli B., Rose M., Perez-Diaz J.-C., Purcell R.,
RA	Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,	RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
RT	Comparative Genomics of Listeria species.;	RT "Comparative genomics of Listeria species.";
Science 294:849-852 (2001).	Science 294:849-852 (2001).	Science 294:849-852 (2001).
CC	-1- FUNCTION: One of the primary rRNA binding proteins. Required for association of the 30S and 50S subunits to form the 70S ribosome, for tRNA binding and peptide bond formation. It has been suggested to have Peptidyl transferase activity; this is somewhat controversial. Makes several contacts with the 16S rRNA in the 70S ribosome (By similarity).	CC -1- FUNCTION: One of the primary rRNA binding proteins. Required for association of the 30S and 50S subunits to form the 70S ribosome, for tRNA binding and peptide bond formation. It has been suggested to have Peptidyl transferase activity; this is somewhat controversial. Makes several contacts with the 16S rRNA in the 70S ribosome (By similarity).
CC	-1- SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the 30S subunit in the 70S ribosome (By similarity).	CC -1- SUBUNIT: Part of the 50S ribosomal subunit. Belongs to the ribosomal protein L2P family.
CC	-1- SIMILARITY: Belongs to the ribosomal protein L2P family.	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ .

SQ	SEQUENCE	277 AA;	30155 MW;	P29296D3EE1E146E CRC64;	KW	Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.	
	Query Match	97.0%;	Score 1412;	DB 1;	Length 277;	SEQUENCE 277 AA;	
	Best Local Similarity	98.2%;	Pred. No. 1.8e-102;			30155 MW; F29296D3EE1E146E CRC64;	
	Matches	274;	Conservative 1;	Mismatches 2;	Indels 2;	Gaps 1;	
Qy	1	MAIKKYKPTINGRGRNMTSLDAETKTTPKSLSLKKPLPKAGRNNOQLTVRHGGHKR	60	Qy	1	MAIKKYKPTINGRGRNMTSLDAETKTTPKSLSLKKPLPKAGRNNOQLTVRHGGHKR	60
Db	1	MAIKKYKPTINGRGRNMTSLDAETKTTPKSLSLKKPLPKAGRNNOQLTVRHGGHKR	60	Db	1	MAIKKYKPTINGRGRNMTSLDAETKTTPKSLSLKKPLPKAGRNNOQLTVRHGGHKR	60
Qy	61	QYRVIDFKRKDGIAKVDISIQDPNRSANIALVYVADGEKRTHCLAPKLEVGQIVES	120	Qy	61	QYRVIDFKRKDGIAKVDISIQDPNRSANIALVYVADGEKRTHCLAPKLEVGQIVES	120
Db	61	QYRVIDFKRKDGIAKVDISIQDPNRSANIALVYVADGEKRTHCLAPKLEVGQIVES	118	Db	61	QYRVIDFKRKDGIAKVDISIQDPNRSANIALVYVADGEKRTHCLAPKLEVGQIVES	118
Qy	121	GADPATDKVGNALPLQNIPTVGTVVHNIEKLKPKGKQGQIARSAGASAQVIGKEKXKVLRSLRS	180	Qy	121	GADPATDKVGNALPLQNIPTVGTVVHNIEKLKPKGKQGQIARSAGASAQVIGKEKXKVLRSLRS	180
Db	119	GAEADIKVGNALPLQNIPTVGTVVHNIEKLKPKGKQGQIARSAGASAQVIGKEKXKVLRSLRS	178	Db	119	GAEADIKVGNALPLQNIPTVGTVVHNIEKLKPKGKQGQIARSAGASAQVIGKEKXKVLRSLRS	178
Qy	181	GIVRMILSTCRATIGQVNGLQHELVNVKGAGRWSRKGTRPRTYRGSVNPNPDHPGGEGR	240	Qy	181	GIVRMILSTCRATIGQVNGLQHELVNVKGAGRWSRKGTRPRTYRGSVNPNPDHPGGEGR	240
Db	179	GIVRMILSTCRATIGQVNGLQHELVNVKGAGRWSRKGTRPRTYRGSVNPNPDHPGGEGR	238	Db	179	GIVRMILSTCRATIGQVNGLQHELVNVKGAGRWSRKGTRPRTYRGSVNPNPDHPGGEGR	238
Qy	241	APIGRPSMSPMGKPTLGRKTRGKSSDKLIVGRKCK 279		Qy	241	APIGRPSMSPMGKPTLGRKTRGKSSDKLIVGRKCK 279	
Db	239	APIGRPSMSPMGKPTLGRKTRGKSSDKLIVGRKCK 277		Db	239	APIGRPSMSPMGKPTLGRKTRGKSSDKLIVGRKCK 277	
<hr/>							
RESULT 4							
ID	RU2_STAAW	STANDARD;	PRT;	277 AA.	RESULT 5	SEQUENCE FROM N.A.	
AC	P60433; Q99S24; Q9AJ03;				Q663774	PRELIMINARY;	
DT	23-MAR-2004 (Rel. 4.3, Created)				AC	P663774;	
DT	29-MAR-2004 (Rel. 4.3, Last sequence update)				DT	05-JUL-2004 (TREMBLrel. 27, Created)	
DT	25-OCT-2004 (Rel. 4.5, Last annotation update)				DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)	
DE	SOS ribosomal protein L2.				DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)	
GN	Name=rplB; OrderedLocusNames=MW2166;				DE	50S ribosomal protein L2.	
OS	Staphylococcus aureus (strain MR2).				GN	OrderedLocusNames=SAS2138;	
OC	Bacteria; Firmicutes; Bacillales; Staphylococcaceae.				OC	Staphylococcus aureus (strain MSSA476).	
OX	NCBI_TaxID=196620;				OC	Bacteria; Firmicutes; Bacillales; Staphylococcaceae.	
RN	[1]				NCBI_TaxID=282459;		
RP	SEQUENCE FROM N.A.				RN	NCBI_TaxID=282459;	
RX	MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;				RX	SEQUENCE FROM N.A.	
RA	Babu T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.,				RA	PubMED=15213324; DOI=10.1073/pnas.0402521101;	
RA	"Genome and virulence determinants of high virulence community-ribosome (By similarity)."				RA	PubMED=15213324; DOI=10.1073/pnas.0402521101;	
RT	Lancet 359:1819-1827(2002).				RA	PubMED=15213324; DOI=10.1073/pnas.0402521101;	
RT	-1- FUNCTION: One of the primary rRNA binding proteins. Required for association of the 30S and 50S subunits to form the 70S ribosome, for tRNA binding and peptide bond formation. It has been suggested to have peptidyl transferase activity; this is somewhat controversial. Makes several contacts with the 16S rRNA in the 70S ribosome (By similarity).				RA	PubMED=15213324; DOI=10.1073/pnas.0402521101;	
CC	-1- SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the 30S subunit in the 70S ribosome (By similarity).				RA	PubMED=15213324; DOI=10.1073/pnas.0402521101;	
CC	-1- SIMILARITY: Belongs to the ribosomal protein L2P family.				RA	PubMED=15213324; DOI=10.1073/pnas.0402521101;	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licenses@isb-sib.ch).				RA	PubMED=15213324; DOI=10.1073/pnas.0402521101;	
CC	EMBL: AP004029; BAB96031.1; -				DR	GO: GO:0005622; C: intracellular; IEA.	
CC	HAMAP: MF_01320; -i; 1; 1.				DR	GO: GO:0015934; C: large ribosomal subunit; IEA.	
CC	InterPro: IPR002171; Ribosomal L2.				DR	GO: GO:1003723; F: RNA binding; IEA.	
CC	IPR005880; IPR005881; Ribosomal L2/b/o.				DR	GO: GO:003735; F: structural constituent of ribosome; IEA.	
CC	InterPro: IPR00894; Nucleic acid OB.				DR	GO: GO:0016740; F: transferase activity; IEA.	
CC	InterPro: IPR002171; Ribosomal L2.				DR	PFAM: PF000642; Protein biosynthesis; IEA.	
CC	InterPro: IPR005880; Ribosomal L2/b/o.				DR	InterPro: IPR00894; Nucleic acid OB.	
CC	Transl SH3-like.				DR	InterPro: IPR002171; Ribosomal L2.	
CC	TIGRFAMs: TIGR01171; rplB_bact; 1.				DR	PFAM: PF03947; Ribosomal L2_C; 1.	
CC	PROSITE; PS00467; RIBOSOMAL L2; 1.				DR	TIGRFAMs: TIGR01171; rplB_bact; 1.	
CC	Complete proteome; Ribosomal protein.				DR	PROSITE; PS00467; RIBOSOMAL L2; 1.	
KW	SEQUENCE 277 AA;				KW	Complete proteome; Ribosomal protein.	
SQ					SQ	30155 MW; F29296D3EE1E146E CRC64;	

Best Local Similarity 98.2%; Pred. No. 1.8e-102; Matches 274; Conservative 1; Mismatches 2; Indels 2; Gaps 1;	DR TIGRFAMS; TIGR01171; rPLB bact; 1.
	DR PROSITE; PS00467; RIBOSOMAL L2; 1.
	KW Complete proteome; Ribosomal protein; RNA-binding; rRNA-binding.
	SQ SEQUENCE 277 AA; 30155 MW; F29226D3EE1E46B CRC64;
Qy 1 MATKCKTPITNGRNM7SLDAETTKTPEKSILKPKAGRNNOQLTRHGGGHKR 60	Query Match 97.0%; Score 1412; DB 1; Length 277;
Db 1 MATKCKTPITNGRNM7SLDAETTKTPEKSILKPKAGRNNOQLTRHGGGHKR 60	Best Local Similarity 98.2%; Pred. No. 1.8e-102; Mismatches 2; Indels 2; Gaps 1;
Qy 61 QYRVIDPFRNKDGINAKYD1QYDPNRSANTIALVYADGERKLYHC1APKGLLEVQTVES 120	Matches 274; Conservative 1;
Db 61 QYRVIDPFRNKDGINAKYD1QYDPNRSANTIALVYADGERKLYHC1APKGLLEVQTVES 118	Qy 1 MAIKKCKTPITNGRNM7SLDAETTKTPEKSILKPKAGRNNOQLTRHGGGHKR 60
Qy 121 GAAIDIKVGNALPLQNTIPVGTVVNLIEKPKGKGQIARSAGASAQVLGKGVYLRLRS 180	Db 1 MAIKKCKTPITNGRNM7SLDAETTKTPEKSILKPKAGRNNOQLTRHGGGHKR 60
Db 119 GAAIDIKVGNALPLQNTIPVGTVVNLIEKPKGKGQIARSAGASAQVLGKGVYLRLRS 178	Qy 61 QYRVIDPFRNKDGINAKYD1QYDPNRSANTIALVYADGERKLYHC1APKGLLEVQTVES 120
Qy 181 GEYRMILSTCRATIGQVENLQHELVNVKAQRGRWKIGTRPTYRGSYVNPNIDPHGGCCEGR 240	Db 61 QYRVIDPFRNKDGINAKYD1QYDPNRSANTIALVYADGERKLYHC1APKGLLEVQTVES 118
Db 179 GEYRMILSTCRATIGQVENLQHELVNVKAQRGRWKIGTRPTYRGSYVNPNIDPHGGCGR 238	Qy 121 GAAIDIKVGNALPLQNTIPVGTVVNLIEKPKGKGQIARSAGASAQVLGKGVYLRLRS 180
Qy 241 APIGRPSMSPMGKPTLGSKCTRGKSSDKLIVTRGRKK 279	Db 119 GAAIDIKVGNALPLQNTIPVGTVVNLIEKPKGKGQIARSAGASAQVLGKGVYLRLRS 178
Db 239 APIGRPSMSPMGKPTLGSKCTRGKSSDKLIVTRGRKK 277	Qy 181 GEYRMILSTCRATIGQVNLQHELVNVKAQRGRWKIGTRPTYRGSYVNPNIDPHGGCGR 240
RESULT 2	Db 179 GEYRMILSTCRATIGQVNLQHELVNVKAQRGRWKIGTRPTYRGSYVNPNIDPHGGCGR 238
RL2_STAN	
ID RL2_STAN	STANDARD;
AC P60432; Q99324; Q9AJ03;	PRT; 277 AA.
DT 29-MAR-2004 (Rel. 4.3; Created)	
DT 29-MAR-2004 (Rel. 4.3; Last sequence update)	
DE 50S ribosomal protein L2.	
GN Name=rPLB; OrderedLocusNames=SA044;	
OS Staphylococcus aureus (strain N315).	
OC Bacteria; Firmicutes; Bacillales; Staphylococcaceae.	
NCBI_TaxID=158879;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;	
RA Kuroda M., Ohta T., Baba T., Uchiyama I., Kobayashi I.,	
RA Cui L., Onuchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,	
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,	
RA Mizutani-Iru Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,	
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yaburaki J.,	
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,	
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,	
RT "Whole genome sequencing of meticillin-resistant Staphylococcus	
RT aureus.";	
RL Lancet 357:1225-1240(2001).	
CC -I- FUNCTION: One of the primary rRNA binding proteins. Required for association of the 30S and 50S subunits to form the 70S ribosome, to have peptidyl transferase activity; this is somewhat controversial. Makes several contacts with the 16S rRNA in the 70S ribosome. (By similarity).	
CC -I- SUBUNIT: Part of the 50S ribosomal subunit. Forms a bridge to the 30S subunit in the 70S ribosome (By similarity).	
CC -I- SIMILARITY: Belongs to the ribosomal protein L2P family.	
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CC EMBL; AF205220; AAC37412.2; -	
CC DR HSSP; P04257; 1RL2.	
CC DR HAMAP; MF 01320; -; 1.	
CC DR InterPro; IPR002171; Ribosomal L2.	
CC DR TIGRFAMS; TIGR01171; rPLB bact; 1.	
CC DR PROSITE; PS00467; RIBOSOMAL L2; 1.	
CC DR Ribosomal protein; RNA-binding; rRNA-binding.	
CC DR InterPro; IPR005880; Ribosomal L2_b/o.	

GenCore version 5.1.6						
Copyright (c) 1993 - 2005 Compugen Ltd.						
MM protein - protein search, using SW model						
run on:	June 9, 2005, 15:49:44 ;	Search time 174 Seconds (without alignments)				
sequence:	1 MAIKKYKPTINGRRNMTSLD.....	KTRRGKKSDFKLIVRGRKKK	279			
coring table:	BLOSUM62					
Gapct	10.0	Gapext	0.5			
searched:	1612378 seqs,	512079187 residues				
total number of hits satisfying chosen parameters:	1612378					
UniProt 03::*	1: uniprot_sprot::*					
	2: uniprot_trembl::*					
post-processing:	Minimum Match 0%					
	Maximum Match 100%					
	Listing first 45 summaries					
database :						
result No.	Score	Query Match Length	DB ID	Description		
1	1412	97.0	277	RL2_STRAW	P60431	staphylococci
2	1412	97.0	277	RL2_STRAAN	P60432	staphylococci
3	1412	97.0	277	RL2_STRAU	P60430	staphylococci
4	1412	97.0	277	RL2_STRAAW	P60433	staphylococci
5	1412	97.0	277	Q6G774	Q6g774	staphylococci
6	1373	97.0	277	Q6GE16	Q6ge16	staphylococci
7	1373	94.3	277	RL2_STAEP	Q8crx3	staphylococci
8	1203	82.6	277	RL2_LISIN	P60425	listeria
9	1203	82.6	277	RL2_LISMO	P60426	listeria
10	1203	82.6	277	Q71WE9	Q71we9	listeria
11	1175	80.7	277	Q65PA4	Q65pa4	bacillus
12	1158	79.5	276	RL2_BACSU	P4919	bacillus
13	1156	79.4	276	RL2_OCPHU	Q8exx9	oceanobacter
14	1154	79.3	276	RL2_BACHD	Q9z911	bacillus
15	1139	78.2	276	RL2_BACAN	Q63h87	bacillus
16	1139	78.2	276	Q63H87	Q63h87	bacillus
17	1139	78.2	276	Q73PP93	Q73F93	bacillus
18	1139	78.2	276	Q6HPQ5	Q6hpq5	bacillus
19	1137	78.1	276	RL2_BACCR	Q81i39	bacillus
20	1125	77.3	275	RL2_BACST	P04257	bacillus
21	1121	77.0	277	RL2_STRP3	Q879x0	streptococci
22	1121	77.0	277	RL2_STRP8	P60435	streptococci
23	1121	77.0	277	RL2_STRPY	P60434	streptococci
24	1120	76.9	276	RL2_ENTFA	Q83951	enterococci
25	1108	76.1	277	RL2_STRPN	Q978v2	streptococci
26	1108	76.1	277	RL2_STPR6	Q8cwv5	streptococci
27	1104	75.8	277	RL2_STRA3	Q8717v5	streptococci
28	1104	75.8	277	RL2_STRA5	Q8e2cb	streptococci
29	1088	74.7	279	RL2_LACP1	Q88xy3	lactobacilli
30	1072	73.6	275	RL2_THTCN	Q8r7v5	thermoanaerobacter
31	1072	70.2	275	RL2_LACI	Q9cdw5	lactococci

ALIGNMENTS

total number of hits satisfying chosen parameters : 1612378

ost-processing: Minimum Match 0% Maximum Match 100%	Listing first 45 summaries
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database : UniProt_03:
 1: uniprot_sprot:
 2: uniprot_trembl:

 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

RESULT 1	
RUL_2	STAAM
ID	RL2
AC	P6043
DT	29-MAR
DT	29-MAR
DT	25-OS
DE	r:
GN	Name=
OS	Staphy-
OC	Bacter-
OX	NCBI_
RN	[1]_-
RP	SEQUEN-
RX	MEDLINE
RA	Kuroda
RA	Cui L.

Result	Query No.	% Match			Length	DB ID	Description
		Score	Match	Length			
1	1412	97.0	277	1	RL2	STAAAM	P60431 staphylococci
2	1412	97.0	277	1	RL2	STAAAN	P60432 staphylococci
3	1412	97.0	277	1	RL2	STAAU	P60430 staphylococci
4	1412	97.0	277	1	RL2	STAAW	P60433 staphylococci
5	1412	97.0	277	1	Q6G774	staphylococci	P60434 staphylococci
6	1412	97.0	277	2	Q6GE16		Q6Ge16 staphylococci
7	1373	94.3	277	1	RL2	STAEP	Q8crq3 staphylococci
8	1203	82.6	277	1	RL2	LISIN	P60425 listeria like
9	1203	82.6	277	1	RL2	LISMO	P60426 listeria like
10	1203	82.6	277	2	Q71We9		Q71We9 listeria like
11	1175	80.7	277	1	Q6SP44		P65pa4 bacillus s
12	1158	79.5	276	1	RL2	BACSU	P42919 bacillus s
13	1156	79.4	276	1	RL2	OCEIH	Q8etx9 oceanobacilli
14	1154	79.3	276	1	RL2	BACHD	Q9z911 bacillus h
15	1139	78.2	276	1	RL2	BACAN	Q81Vz7 bacillus a
16	1139	78.2	276	2	Q63H87		Q63nH7 bacillus c
17	1139	78.2	276	2	Q73F93		P73E53 bacillus c
18	1139	78.2	276	2	Q6HPQ5		Q6hpq5 bacillus t
19	1137	78.1	276	1	RL2	BACCR	Q81Jz9 bacillus c
20	1125	77.3	275	1	RL2	BACST	P04257 bacillus s
21	1121	77.0	277	1	RL2	STRP8	Q879r0 streptococci
22	1121	77.0	277	1	RL2	STRP8	P60435 streptococci
23	1121	77.0	277	1	RL2	STRPY	P60434 streptococci
24	1120	76.9	276	1	RL2	ENTPA	Q8399g1 enterococci
25	1108	76.1	277	1	RL2	STRPN	Q97Bv2 streptococci
26	1108	76.1	277	1	RL2	SPR86	Q8crv5 streptococci
27	1104	75.8	277	1	RL2	STRA5	Q8e7L5 streptococci
28	1104	75.8	277	1	RL2	STRA5	Q8e2C8 streptococci
29	1098	74.7	279	1	RL2	LACP1	Q88xy3 lactobacilli
30	1072	73.6	276	1	RL2	LACI2	Q9cdcv5 lactococci
31	1022	70.2	275	1	RL2	THETN	Q8r7v5 thermoanaerobacter